HUMAN HEALTH

ENVIRONMENTAL HEALTH

ChemBio3D 13.0 User Guide

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What's New

ChemBio3D 13.0 introduces a variety of improvements and new features not found in earlier versions. The new features are briefly described below.

Support for GAMESS 09. ChemBio3D 13.0 comes with GAMESS 09 installed. For more information, see "CS GAMESS" on page 133.

Depiction and animation of GAMESS IR Vibrations. After you compute an infrared spectrum, you can view and animate the IR vibration modes and the vectors that are applied. For more information, see "Viewing and animating GAMESS IR vibrations" on page 136.

Molecular Orbital Calculations using GAMESS 09 and MOPAC 2009. You can now calculate molecular orbitals using either GAMESS 09 or MOPAC 2009. By default, PM6 is the basis set in the latest version of MOPAC.

Support for Gaussian 09. In addition to Gaussian 03, ChemBio3D also supports Gaussian 09. Gaussian can be purchased from PerkinElmer.

2D projections of 3D surfaces. The volume slicing tool lets you view a two-dimension cross section of almost any molecular surface. This becomes quite useful for viewing the electron density at any location in your model. You can slice through an orbital or an entire model in either the X-, Y-, or Z-planes and adjust the location of the slice as desired. For more information, see "Volume slicing" on page 70.

Dropbox integration. ChemBio3D 13.0 provides an interface to Dropbox service to users with a valid Dropbox account. You can upload and download files between your remote Dropbox folder and your local machine. For more information, see Dropbox interface. Dropbox plug-in can be downloaded from the Dropbox Web site.

Docking. AutoDock helps you determine how one or more small molecules may be arranged to fit inside the cavity of a larger molecule. You choose the molecules, the cavity binding sites, and calculation parameters. AutoDock calculates and displays the conformers and positions of each small molecule that fit your requirements.
For more information, see "Docking" on page 155.

CONFLEX. CONFLEX is a conformational analysis package developed by the CONFLEX Corporation. Using CONFLEX, you can search for low energy conformers of a model and create a fragment for each one in its optimal state.
For more information, see "CONFLEX" on page 109.

Molecular Networks integration. ChemBio3D incorporates new features from Molecular Networks for determining pKa, LogS and LogP solubility properties. See "ChemBio3D properties" on page 216. Also see "About Molecular

Networks" on page 2.

About ChemBio3D 13.0

ChemBio3D 13.0, a part of the ChemBioOffice 2012 suite lets you build, visualize, and analyze 3D models of chemical structures. ChemBio3D 13.0 models can be imported into desktop publishing tools or displayed on the Web. ChemBio3D 13.0 comes with GAMESS, an ab initio quantum chemistry package. GAMESS Lets you predict UV/VIS, IR and NMR spectra, calculate energy and a number of other molecular properties.

Additional computational engines

ChemBio3D supports several additional computational engines. These tools are briefly mentioned below. Their full descriptions are found in respective chapters of this guide. For availability and purchase information, contact PerkinElmer Informatics.

About Gaussian

ChemBio3D supports Gaussian 03 and Gaussian 09. Gaussian is a property prediction program used by chemists, chemical engineers, biochemists, physicists, and other scientists. Using the *ab initio* and semi-empirical quantum mechanics, Gaussian predicts the energies, molecular structures, vibrational frequencies and chemical properties of molecules and reactions in a variety of chemical environments. You can apply Gaussian to both stable compounds and compounds that are difficult or impossible to observe experimentally such as short-lived intermediates and transition structures. Gaussian supports *ab initio* methods, such as restricted and unrestricted Hartree Frock methods. You can use *ab initio* and semi-empirical methods for calculating electron density surface and molecular geometry optimization. Gaussian supports ground state semi-empirical methods such as CNDO/2, INDO, MINDO3, and MDO energies and gradients.

Note: *The term "semi-empirical" refers to methods that use the general process dictated by quantum mechanics, but simplify it to gain speed and later use experimental data to compensate for the simplification.*

Note: *Gaussian 03 requires 32-bit version of Windows and Gaussian 09 requires either 32-bit version or 64-bit version of Windows.*

See "Gaussian" on page 104 for more information.

About CS MOPAC

CS MOPAC performs semi-empirical calculations on atoms and molecules to determine details of molecular structures and properties. For example, with CS MOPAC you can perform thermodynamic calculations, geometry optimizations, and force constant calculations. CS MOPAC provides the functionalities of MOPAC through the ChemBio3D interface. ChemBio3D supports MOPAC 2007 and MOPAC 2009.
There are two CS MOPAC options available: CS MOPAC Ultra and CS MOPAC Pro.
CS MOPAC Ultra includes all the capabilities of MOPAC, and is available only as an optional plug-in. CS MOPAC Ultra provides support for advanced features, such as MOZYME and PM5 methods.

With CS MOPAC Pro, you can perform simple and advanced energy minimizations, optimize to transition states, and compute various properties. Both CS MOPAC Pro and CS MOPAC Ultra supports MOPAC sparkles. For more information, see "MOPAC" on page 110.

***Note:** "MOPAC sparkles" are the extra eight elements added to MOPAC that represent pure ionic charges.*

CS MOPAC is included in some versions of ChemBio3D 13.0 or may be purchased as an optional plug-in. Contact PerkinElmer Informatics or your local reseller for details.

About AutoDock

AutoDock is an automated docking tool that helps you predict how small molecules bind to a receptor of known 3D structure. ChemBio3D maintains an interface to AutoDock to perform the docking calculation. AutoDock calculations are performed in several steps. For further information, please visit http://autodock.scripps.edu
See Docking for more information.

About CONFLEX

CONFLEX is a conformational analysis package developed by the CONFLEX Corporation. Using CONFLEX, you can searche for chemically significant conformers in flexible molecules and displays the conformers as fragments in your model. Conformers are reported based on the search method and energy limit that you define. For further information, please visit www.conflex.us
See CONFLEX for more information.

About Molecular Networks

pKa, logS and logP for predicting acid dissociation constants, aqueoues solubility and octanol/water distribution coefficients of chemical compounds are computational calculator modules based on Molecular Networks' chemoinformatics platform MOSES. MOSES is developed, maintained, and owned by Molecular Networks GmbH, Erlangen, Germany. For further information please visit www.molecular-networks.com/moses. All rights reserved. Molecular Networks GmbH, Erlangen, Germany (www.molecular-networks.com).

Limitations
Only the following atom types and hybridization states are parameterized:

$C_{sp}3$	$N_{sp}2$	$O_{sp}2$	$S_{sulfone}$
$C_{sp}2$	N_{amide}	$P_{sp}3$	F
$C_{aromatic}$	$N_{aromatic}$	$S_{sp}3$	Cl
C_{sp}	N_{sp}	$S_{sp}2$	Br
$N_{sp}3$	$O_{sp}3$	$S_{sulfoxide}$	I

Serial numbers and technical support

The serial number is a unique key that helps you install and activate the ChemBioOffice application on your computer. This serial number is displayed on the outside of the original application box. This is the same number you entered when you launched your ChemBioOffice application for the first time. If you have thrown away your box and lost your installation instructions, you can still find the serial number from the application. Go to **Help** > **About ChemBio3D**.The serial number appears in the dialog box.

For more information on obtaining serial numbers and registration codes see the online Services Web site.

Technical support is available to registered users through the Internet and our Technical Support department.When contacting Technical Support, always provide the serial number and version number of your ChemBioOffice application. Our Technical Support Web pages contain answers to frequently asked questions (FAQs) and other information.

To access our Technical Support in ChemBio3D, go to **Online**>**Browse CambridgeSoft Technical Support**.
If you are unable to find a solution on the Web site, follow these steps before you contact Technical Support:

1. Check the system requirements for the software.
2. Read the Troubleshooting section and follow the possible resolution tactics outlined there.
3. If all your attempts to resolve a problem fail, contact technical support.

- Try to reproduce the problem before contacting us. If you can reproduce the problem, please record the exact steps.
- Record the exact wording of any error messages that appear.
- Record what you have tried to correct the problem.

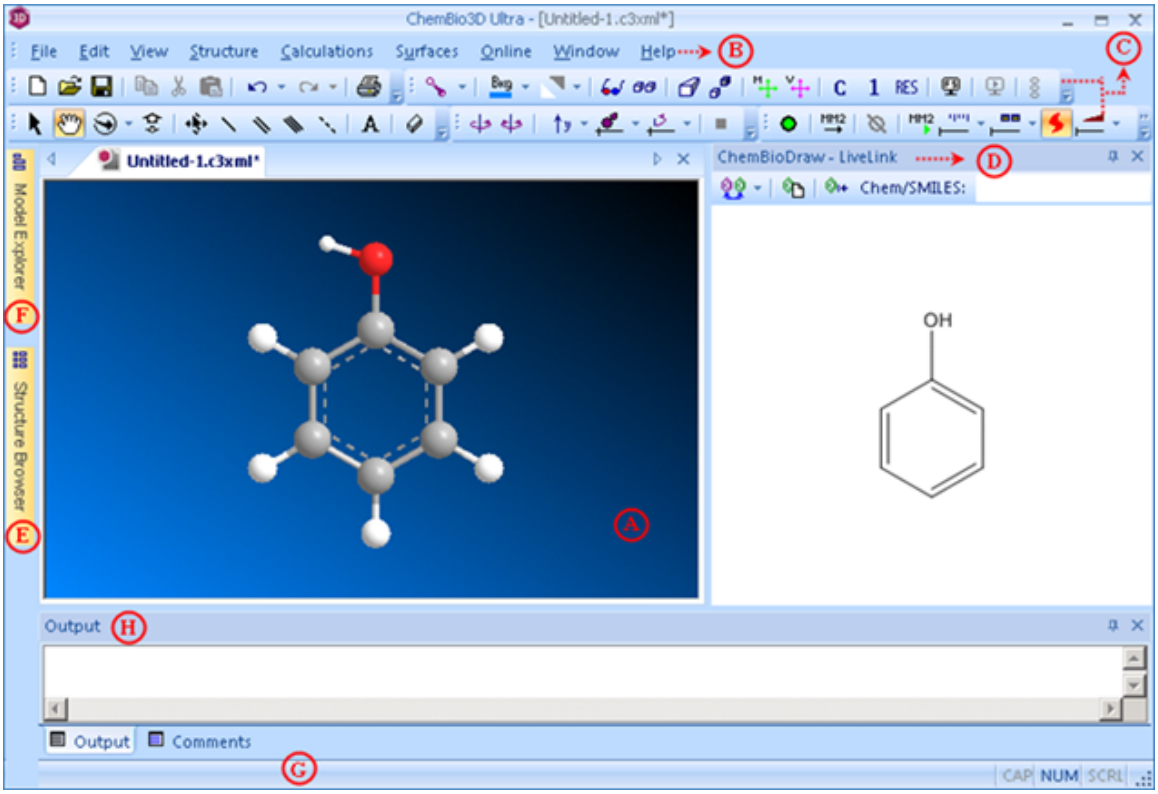
Note: *The AutoDock and computation engines are third-party products and may produce log files for the functions you run. Refer to the log file to determine whether an issue you encounter is due to the third-party product or ChemBio3D and provide this information when you contact technical support.*

ChemBio3D 13.0 Basics

For the basic information about ChemBio3D functionality and use, please follow the links below.
Getting around. Learn where things are on screen.
Basic Model Building. Learn to build your first model.
Tutorials. Follow demonstrations on how to perform tasks in ChemBio3D.
Computational Engines. Learn what computation methods are available in ChemBio3D.

Getting around

This section describes the Graphic User Interface (GUI), with its various screen elements, and its use.



The main screen: A) Model window; B) Main menu; C) Toolbars; D) ChemDraw panel tab; E) Structure Browser tab; F) Model Explorer tab; G) Status bar; H) Output window.

Model window. The work space where you build and view models.
Main menu. Includes all tools necessary for building and viewing models, running calculations, and displaying chemical properties. Many of the menu options are also available in context menus.
Toolbars. Contain icons that offer shortcuts to many commonly used functions. You can click-drag the toolbars to anywhere on your screen.

ChemDraw panel. Lets you create or modify drawings of your model in two dimensions.
Structure Browser. Lets you browse through the list of structures and view each one in the Model window.
Model Explorer. Displays a hierarchical tree representation of the model. The model explorer is useful for working with complex molecules such as proteins.
Status bar. Displays information about the active frame of your model and hidden atoms.
Output window. Displays text results such as calculation results.

The model window

You build your models in the model window. Each model file you open or create adds a new tab. Select a tab to activate the model you want to view. An asterisk next to the file name indicates that the file has not been saved since you last made changes to it.

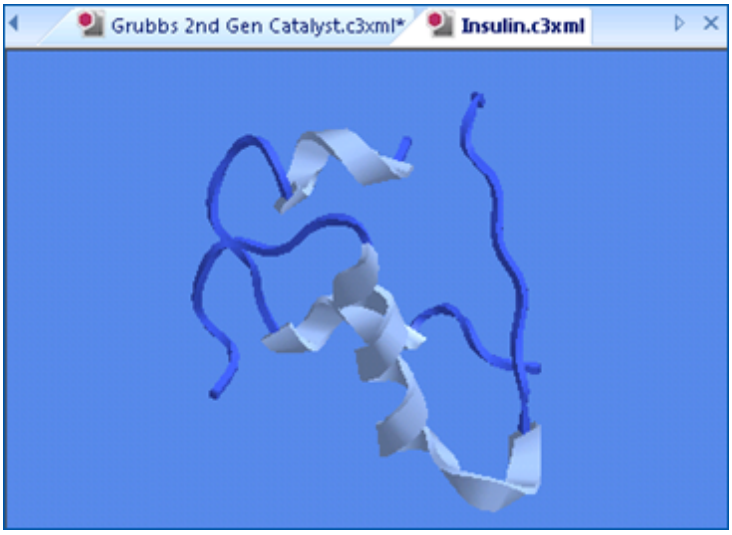


Figure 2.1: A model of insulin in the active tab.

The ChemDraw panel

Using the ChemDraw panel, you can draw 2D structure drawings and convert them to 3D models. Alternatively, you can build a 3D model and convert it to a 2D drawing that displays in the panel. To activate the ChemDraw panel, go to **View>ChemDraw Panel**. By default, the panel opens on the right side of the screen. You can also float the panel anywhere on your screen or dock it to the ChemBio3D user interface. Right-click the ChemDraw panel title bar and select either **Docking** or **Floating**.You can also click on the ChemDraw panel title bar and drag it to any of the standard docking orientations.

Linking the 2D and 3D Views

The ChemDraw panel and model window have two linking modes, LiveLink and Insertion. In LiveLink mode, any model you build in the model window appears in the ChemDraw panel. Conversely, any structure you draw in the ChemDraw panel appears in the model window. The ChemDraw panel title bar shows which mode is active.
The linking options appear just below the title bar. Insertion mode options are:

Link Mode. toggle between LiveLink mode and Insertion mode.
Clear. clear the structure in the ChemDraw panel.
Add or Replace contents in ChemDraw panel. the default function is to replace.
Chemical names/SMILES. create a model by typing a compound name or SMILES string into the Name=Struct box.
Group name. specify the group name of the compound to be added or replaced.
Group ID. specify the group ID of the compound to be added or replaced.
Draw->3D (ADD). This option is available if these conditions are met:

- A valid Group name and Group ID for the compound is specified.
- A structure appears in the ChemDraw-Insertion Panel.
- The specified ID value is numeric.

To draw a structure using Draw->3D (ADD):

1. Specify the group name and group ID of the compound.
2. Click the **Draw->3D (ADD)** icon.

If a structure with specified group name/ group ID combination exists, a message appears prompting you to replace the existing structure in the model window with the new one. To replace the existing structure, click **Yes**. The new structure replaces the existing structure in the model window and in the structure browser. If the structure browser is currently activated, the value is added to the structure browser.
If no structure with specified group name/ group ID combination exists, the structure in the ChemDraw panel is added to the model window and the structure browser.

ChemDraw panel synchronization limits
By default, the LiveLink mode is available only for molecules of fewer than 200 atoms.
To change the default setting:

1. Go to **File**>**Preferences**. The ChemBio3D Ultra Preferences dialog box appears.
2. Click the **ChemDraw** tab.
3. Specify the number of atoms in **Atom Synchronization Limit (100-10000)**.
4. Click **Apply** and click **OK**.

Note: *A higher value in the* ***Atom Synchronization Limit (100-10000)*** *field slows down the drawing as large diagrams have to be generated.*

Structure browser

Using the Structure Browser, you can browse through multiple structures stored in a file and view them in the model window. As you browse through a model, you can select in the structure browser which structures appear in the model window and even overlay the structures. This is useful for tasks such as examining drug-like molecules and their interactions within a receptor.
By default, the Structure Browser is collapsed and appears as a vertical tab left of the model window. Hover the mouse over the tab to display the Structure Browser.

To import structures into the structure browser:

1. Go to **File**>**New** to open a new document window.
2. Go to **File**>**Import File** to import a file that contains the structures to view.

Note: *You can import structural data from either an SD file, sybyl mol2 file, sm2 file,or an ml2 file.*

After you import the file, the structures from the file are listed as fragments in the model explorer. To browse the structures, you must first drag the structures from the model explorer into the structure browser:

1. Click the auto hide icon, in the model explorer and in the structure browser windows so that both windows remain open.
2. Click and drag a fragment from the model explorer window into the structure browser window. The structure names are copied to the structure browser.
3. Drag more fragments as desired from the model explorer to the structure browser.

To view or hide each structure in the structure browser, select or de-select its corresponding check box.

- a check in the box indicates the structure is in view.
- an empty box indicates the structure is hidden.
- a gray box indicates the structures is selected. The selected structure is always in view.

Tip: *To copy all fragments, right-click in the structure browser and select* ***Auto-populate the Structure Browser****.*

Note: *If you delete the fragment in the model explorer, the fragment is also removed from the structure browser.*

Fast overlay

To overlay all objects, right-click in the structure browser and select **Fast Overlay**. The fragments in the structure browser are overlayed.

MM2 calculations

You can run simple MM2 calculations on fragments listed in the structure browser. Calculations can only be run on one fragment at a time.

To perform an MM2 minimization on a fragment, right-click the fragment and select **MM2 Minimization**.

You can also simulate the rotational and translational kinetic energy in fragments over a range of temperatures. Right-click the fragment and select **MM2 Dynamics**. The results of the simulation are listed in the Output window.

Display options

To change the display mode for a fragment:

1. Right-click the fragment in the structure browser.
2. In the context menu, go to Display Mode and select display mode option. For more information, see "Display modes" on page 34.

Color

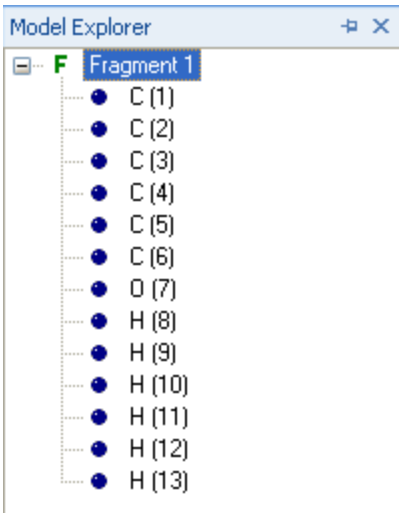
To apply the same color to all atoms in a fragment:

1. Right-click the fragment in the structure browser and go to **Color**>**Select Color**. A color palette opens.

2. In the color palette, choose the color you want and click **OK**.

Model explorer

The model explorer lets you explore the structural features of the model. By default, the model explorer is collapsed and appears as a vertically aligned tab. When you hover the mouse over the model explorer tab, the model explorer window appears and displays a hierarchical tree representation of the currently displayed model:



Using the Model Explorer window, you can alter the model properties. The changes you make to a group are applied to all members in the group.
The hidden or changed features are marked with colored icons, so you can track your modifications. For more information, see "Model Explorer" on page 51.

User interface preferences

You can change the user interface style and behavior to suit the way you work. You can change the GUI color scheme, tab behaviors, and other display options.
To change the settings:

1. Go to **File**>**Preferences**. The **Preferences** dialog box appears.
2. Click the **GUI** tab.
3. Choose a style in the **GUI Style** section to change the overall look and feel of the ChemBio3D interface.

   Note: *The VS 2005 (Whidbey) style option includes smart docking for toolbars.*

4. Click **Apply** to view the new settings. To return to the default style setting, click **Reset to Default**.
5. Enable or disable any of the following features under the **Window Settings** section.
   - Tabbed windows. This enables each open file to be represented as a tab in the model window.
   - Sliding windows. This enables other windows such as Structure Browser, and Model Explorer to slide in and out of the ChemBio3D. If unchecked, the windows will appear or disappear with no sliding.

- Sliding window animation. This enables animation for the sliding window.
- Message in Output box. This displays message in the Output box at the bottom of the ChemBio3D.

Note: *You may need to close and restart ChemBio3D to activate these features.*

6. Click **OK**.

Background settings

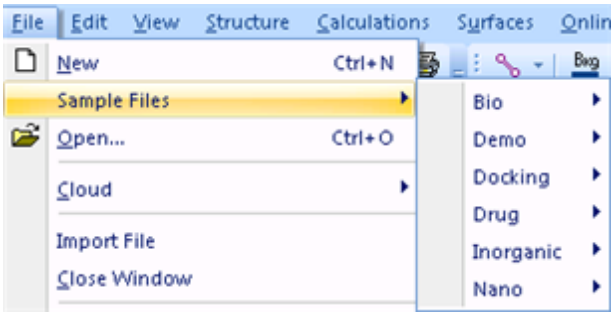
To set background color, effects, and picture, go to **File**>**Model Settings**>**Background** tab. Your changes apply only to the current model window unless **Set as Default** is clicked.

Sample files

ChemBio3D includes a variety of sample files to help you learn how to build and study molecular models, including biological and inorganic structures.

To open a sample file, go to **File**>**Sample Files** and select a file from one of the following groups:

- Bio
- Demo
- Docking
- Drug
- Inorganic
- Nano



Dropbox interface

ChemBio3D 13.0 provides an interface to Dropbox service. Dropbox service when accessed through ChemBio3D 13.0 interface, serves as a cloud repository for files. To use the Dropbox service, you must have:

- A valid Dropbox account, and
- ChemBio3D 13.0 installed.

You can upload your drawings from the current ChemBio3D document windows to your remote Dropbox folder location. You can later download these files when required.

Signing into Dropbox

When accessing Dropbox from ChemBio3D 13.0 for the first time, you need to authorize ChemBio3D's interaction with Dropbox folder. To do so:

1. Go to **File>Cloud>Dropbox>Sign In**. The '**Enter Dropbox User Name**' dialog box appears.

Enter Dropbox User Name
jsmith@hotmail.com
Force re-authorization of this application
Internet connection confirmed
OK
Cancel
This application will never ask you for your Dropbox password.
Your username is used as part of the authorization of this application
to access Dropbox.

2. Enter your Dropbox username and then click **OK**. The Authorization Confirmation dialog box appears.
3. Click **OK**. The Cloud Linking Confirmation window appears.
4. Enter your Dropbox account email address and password. Click **Sign in**.
5. Click **Allow**. The Cloud Linking Confirmation window displays a success message.
6. Click **OK**.

You need to authorize ChemBio3D's interaction with Dropbox folder only when you access Dropbox from ChemBio3D 13.0 for the first time. However, you can choose to re-authorize ChemBio3D's interaction with Dropbox folder anytime by selecting the **Force re-authorization of this application** checkbox in the Enter Dropbox User Name dialog box.

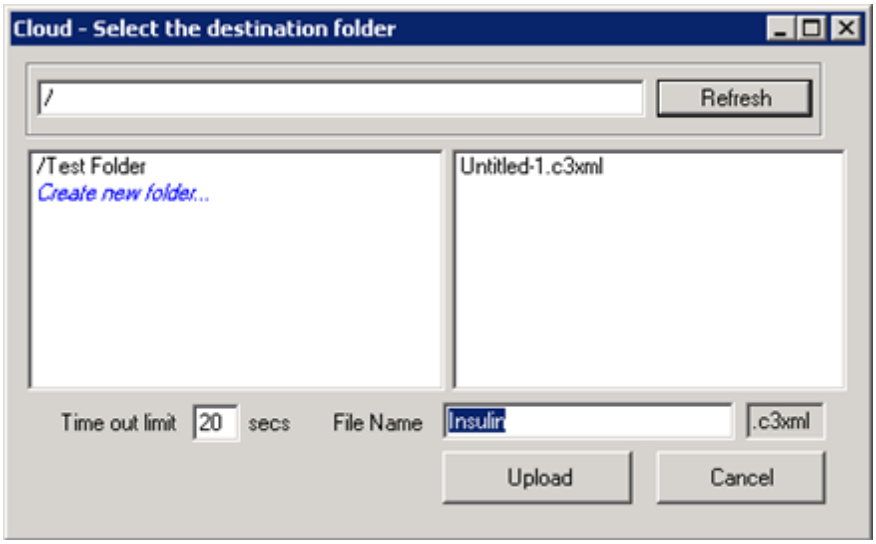
For all subsequent sign-in, do the following:

1. Go to **File>Cloud>Dropbox>Sign In**. The 'Enter Dropbox User Name' dialog box appears.
2. Enter your Dropbox account email address and password.
3. Click **OK**. The options to Upload, Download, and Sign out are enabled in ChemBio3D 13.0.

Upload files

You can upload your drawing in the current document window in ChemBio3D 13.0 to your remote Dropbox folder. To upload a file:

1. Go to **File > Cloud>Dropbox>Upload As**. The 'Cloud Upload' dialog box appears.
2. Specify the name of the file.
3. Select the file format in which you want to upload the drawing.
4. Click **OK**. The Cloud - Select the destination folder dialog box appears.



5. Select a folder location to save the file. You can create a new folder by either double-clicking within the folder list column, or double-clicking the **Create new folder** link.Specify the new folder name, and click **OK**.
6. (optional) If you want to change the file name, enter the new file name in the File name textbox at the bottom of the dialog box.
7. (optional) Specify a time limit for the upload process to complete, by specifying a value in 'seconds' in the Time out limit textbox. You can specify any value between a minimum of 5 seconds and a maximum of 120 seconds as the time out limit.
8. Click **Upload**.

Download files

You can download the files from your remote Dropbox folder to your local machine. When download is complete, the drawing automatically appears in the ChemBio3D document window. You can save the file in a desired location.

To download a file:

1. Go to **File > Cloud>Dropbox>Download**.The 'cloud-select the destination folder' dialog box appears.
2. Do one of the following:
   - Double-click the file that you want to download.
   - Browse to a file that you want to download and click **Download**.

Note: *You can specify a time limit for the download process to complete, by specifying a value in 'seconds' in the Time out limit textbox. You can specify any value between a minimum of 5 seconds and a maximum of 120 seconds as the time out limit.*

Basic Model Building

A model can consist of one or more molecular structures, solvents, ions, or just one atom. There are several basic ways to build a model:

- Build the model one bond at a time using the model building tools. See "Using bond tools" on page 13.
- Draw a 2D structure in the ChemDraw panel and convert the structure to a 3D model. See "The ChemDraw panel" on page 5.
- Enter the name of the chemical structure into the model window using the Build from Text tool. See "Building from text" on page 16.
- Enter a chemical name or SMILES in the ChemDraw panel.
- You can also build models by importing model data from a table. See "Building with Cartesian tables" on page 85.

Usually, a combination of these methods yields the best results. For example, you might build a carbon skeleton of a model in the ChemDraw panel or with the bond tools, then change some of the carbons into other elements using the Build from Text tool.
After building a basic model, you may wish to explore some of the basic ChemBio3D features. For example, you can move, hide, and resize objects. For better viewing, you can also rotate, move, and scale your model.

Default settings

If you are new to ChemBio3D, we recommend that you choose the default settings and an appropriate display mode. It is suggested to choose Ribbon or Cartoons display mode for protein molecules and Wire Frame or Ball and Stick display mode for large molecules. You may choose any display mode for small molecules as they render well in any display mode. The appearance of the models depends on the selected display mode.
To apply the default settings:

1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. Click **Reset to Default**.
3. Click **OK**.

Selecting a display mode

Choosing the cylindrical bonds display mode ensures that your models look similar to what you see in this guide.
To select the display mode, do one of the following:

- Go to **View**>**Model Display**>**Display Mode**>**Cylindrical Bonds**.
- On the Model Display toolbar, click the drop-down arrow next to and select **Cylindrical Bonds** from the drop-down list.

> ***Note:*** *To activate the Model Display toolbar, go to* ***View>Toolbars>Model Display****.*

For more information, see Display modes.

Using bond tools

Use the bond tools to create the basic structure of your models. Subsequently, you can modify it to look the way you want. For example, you can change the carbons or hydrogens to other elements or hide the hydrogens to reduce clutter on the screen.

Figure 3.1: The Building toolbar includes the single, double, triple, and dummy bond tools.

To create a model using bond tools:

1. Choose a bond tool, such as the Single Bond tool.
2. In the Model window, click and drag in the direction you want the bond to be oriented.
3. Release the mouse button to complete the bond.
4. To add more bonds, click and drag from an atom you just drew.
5. To change an atom, click it with the Build from Text tool selected, and enter the new atom symbol. For example, to change a hydrogen atom to a chlorine atom:
   a. Click the hydrogen atom. A text box appears.
   b. Type Cl in the text box.
   c. Press ENTER.

Changing bond order

To change the bond order of one or more bonds at a time, you can use the bond tools, commands, or the Build from Text tool. (You can also change the bond order for bonds attached to an atom by changing the atom type. See "Building types " on page 140.)

Changing bond order with a bond tool

To change the bond order with a bond tool:

1. Select a bond tool (of a different order).
2. Click-drag from one atom to another atom.

Changing bond order using command

To change the bond order using a command:

1. Right-click a bond. The bond will turn to yellow color.
2. Point to **Set Bond Order**, and choose a bond order.

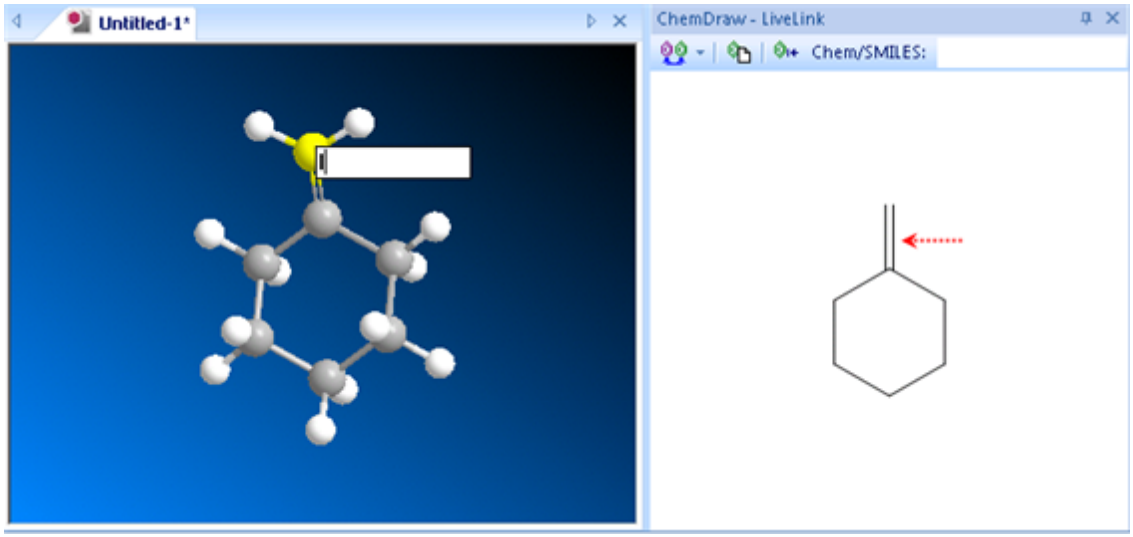
Changing bond order by changing the type of an atom at one of the bond extremes

This method is applicable only if you change a higher bond order to a lower bond order. If you apply this method to change a lower bond order to a higher bond order, a single bond is generated and valency is completed with hydrogens.

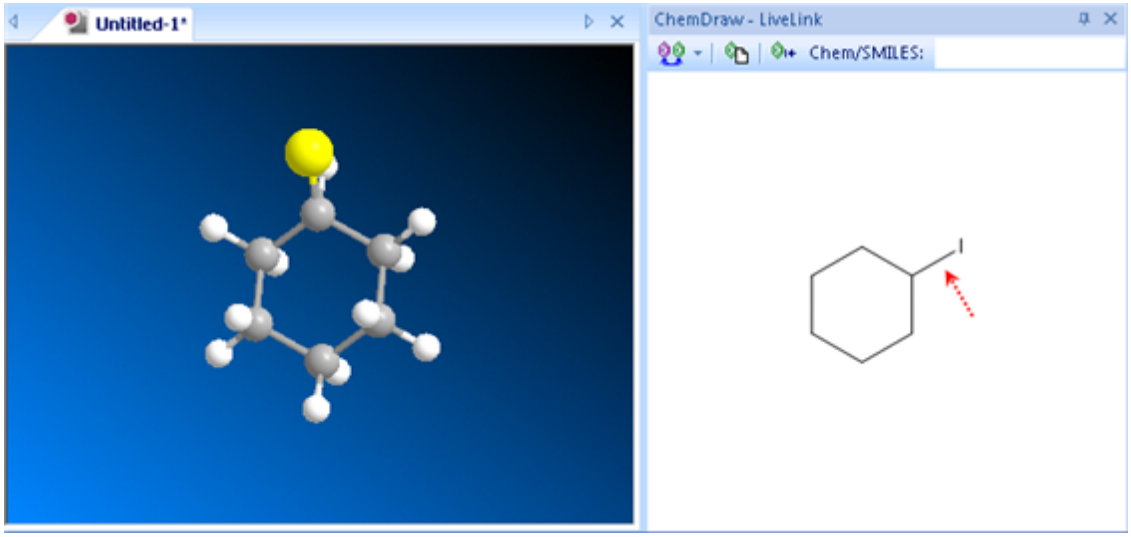
To change the bond order by changing an atom type on any end of the bond:

1. Click the Build from Text tool.

2. Click the atom that is attached to the bonds whose order you want to change.
3. Enter the new atom type that will replace the selected atom. In the following example, we are replacing the Carbon (C) by an Iodine (I).



4. Press ENTER. The bond order of the bond changes to reflect the new atom type.



Changing several bonds at once

To change several bonds at once:

1. Open the ChemDraw panel and click in it to activate the ChemDraw control.
2. Choose either the Lasso or Marquee tool.
3. SHIFT+click the bonds to change.
4. Right-click in the selected area, and do one of the following:
   - Click **Single** and select a bond type.
   - Click **Double** and select a bond type.

- Click **Triple** and select Plain.

5. Click in the ChemBio3D window to complete the action.

Note: *To break a bond, right-click the bond and select* ***Break Bond****.*

Creating rings

To create a ring using the bond tools:

1. Select a bond tool.
2. Click-drag from one atom in a structure to a nonadjacent atom in the same structure.

Note: *In general, this will lead to distorted structures and MM2 or MMFF94 minimization will be needed to fix this.*

Using the ChemDraw panel

Using the ChemDraw panel, you can draw two-dimensional structures in the same way as you would in Chem-BioDraw. Alternatively, you can build models with text using the Chem/SMILES box of the ChemDraw panel. As you draw your structure, the corresponding 3D model appears in the Model window.
To build a model using the ChemDraw panel:

1. Go to **View**>**ChemDraw Panel.** The ChemDraw panel appears.
2. Click in the panel to activate it. The Tools palette appears.

   Note: *If you don't see the Tools palette, right-click in the ChemDraw panel, and select* ***View>Show Main Toolbar****.*

3. Select a tool in the Tools palette and click in the ChemDraw panel to draw structure using the selected tool. With the ChemDraw panel LiveLink option selected (in the upper left corner of the ChemDraw panel), the corresponding 3D model appears in the model window as you draw your structure.

Alternatively, you can draw a structure using ChemBioDraw and paste the structure into the ChemDraw panel:

1. Draw a structure in ChemBioDraw.
2. Copy the structure to the clipboard.
3. In ChemBio3D, go to **Edit**>**Paste** or type CTRL+V in the ChemDraw panel.

For more information, see The ChemDraw panel.

Using other 2D drawing packages

In ChemBio3D, you can also use 2D structures drawn in 2D drawing packages other than ChemDraw. When you draw models using these packages:

- The standard measurements are applied to the model. For more information, see "2D to 3D Conversion" on page 248.
- ChemBio3D ignores objects, such as arrows, orbitals, and curves copied to the clipboard.
- Superatoms in ISIS/Draw are expanded if ChemBio3D finds a corresponding substructure. Otherwise, you must define a substructure. See "Defining substructures" on page 24.

Building from text

A simple way to create a model is to enter a text string that represents the structure for the model you want to build.

You can enter the text as either the structure name, formula, InChI, or SMILES string.

Here are a few examples:

- Name: `Tyrosine`, `Iron (III) Phosphate`
- Formula: `CH3CH2COOPH2`, `CH3(CH2)2COO-NH4+`
- SMILES string: `OC[C@@H](O1)[C@@H](O)[C@H](O)[C@@H](O)[C@@H](O)1`
- InChI string: `InChI=1/C8H7ClO/c1-6(10)7-2-4-8(9)5-3-7/h2-5H,1H3`

A model can consist of multiple structures. Each structure is defined as a fragment[1].

Note: Water is considered a solvent. Each water molecule you add to your model constitutes one fragment.

Using the Name-to-Structure (N2S) tool

To build a model from text:

1. Select the Build from Text tool, on the Building toolbar.
2. Click in the model window. A text field appears.
3. In the text field, either type or paste the name of the structure and press ENTER.

Tip: Here are several tips to keep in mind while using the text tool to build models:
1. Text is case sensitive. For example, to specify an oxygen atom, type O.
2. You can add a formal charge using text. For example, type PhO- to create a model of a phenoxide ion instead of phenol.
3. When you double-click an atom, the content of the previous text box are applied to that atom. If several atoms are selected, The contents of the text box are applied to each atoms independently.
4. Not all text substitutions make sense. For example, selecting two atoms in the same chain with a label of "benzene" will not work.

The interpretation of the text in a text box depends on whether atoms are selected as follows:

- If nothing in the model window is selected, a new molecule is added.
- If one or more atoms selected, the text is added to the selection unless the specifications for the selected atom are violated.
- When a text box is visible, you can modify the selection by SHIFT+clicking or SHIFT-dragging across atoms.

You can also change building types and specify order of attachment.

The Build from Text tool lets you enter text either directly or using the Table editor.

---

[1]Ionic compounds may consist of multiple fragments—one for each ion.

📝 ***Note:*** *For all discussions below, all the Model Building tab options in the Model Settings dialog box are assumed to be turned on.*

Using symbols and formulae

Using the Build from Text tool, you can use chemical symbols and formulae to build models.

To use an element symbol:

1. Select the Build from Text tool.
2. Click in the model window and type `C`.
3. Press ENTER. A model of methane appears.

The atom type is assigned as C Alkane and the appropriate number of hydrogens are added.

To use the same text to add another methyl group:

1. Point to the atom you want to replace, in this example a hydrogen, and click. The text box appears with the previous label.
2. Press ENTER.

To add a different element:

1. Click a hydrogen atom. A text box appears over the atom.
2. Type `N` and press ENTER. A nitrogen is added to form ethylamine.

To build ethylamine in one step:

1. Click in the model window. A text box appears.
2. Either type `CH3CH2NH2` or `ethylamine`.
3. Press ENTER.

The Table editor

To build models using the Build from Text tool, you can use the Table editor to enter text instead of typing the text.

To use the Table editor to enter text:

1. Go to **View**>**Parameter Tables**>**Chem3D Building Atom Types**.
2. Select the element or building type in the table.
3. Press CTRL+C.
4. Double-click in the ChemBio3D Model Window.
5. In ChemBio3D, go to **Edit**>**Paste**.
6. Press ENTER.

Building models from SMILES strings

To build models from names, using the Chem/SMILES box, do one of the following:

- In the Chem/SMILES box, enter a chemical name or a SMILES string and press ENTER.
- Copy a name or SMILES string from a document, paste it into the Chem/SMILES box, and press ENTER.

Tip: *You can paste a name or SMILES string into the Model window to draw a 3D model. You can also paste chemical formulae into the ChemBio3D Model window. Be aware, however, that a formula may represent an isomer.*

By default, the ChemDraw panel replaces existing structures if you use the Chem/SMILES box to draw structures. To ensure that existing structures are not replaced while you draw structures using the Chem/SMILES box, click Add or Replace contents of ChemDraw panel tool .

Adding fragments

A model can comprise several fragments. Typically, a fragment consists of one structure in your model[1].
To add a fragment using the Build from Text tool:

1. Click in an empty area of the window. A text box appears.
2. Type the name of an element, atom type, or substructure, such as H2O for water.
3. Press ENTER. The fragment appears.
4. (Optional) Double-click a different location to add another fragment.

Note: *Water is considered a solvent. Each water molecule you add to your model constitutes one fragment.*

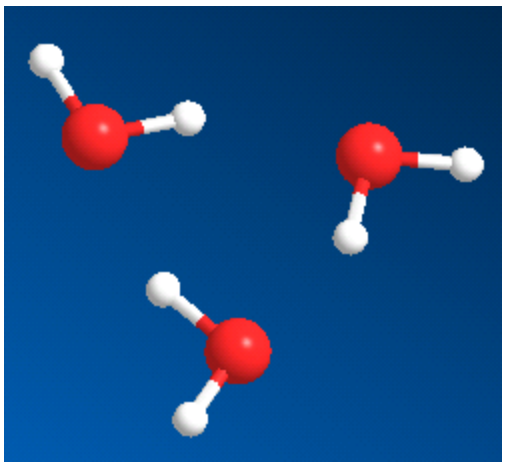


Figure 3.2: Three fragments of an H2O model.

Selecting atoms and bonds

Typically, you must select atoms and bonds before you modify or move them.
To select an atom or bond in the display window:

1. Click the **Select** tool.
2. Click the atom or bond.

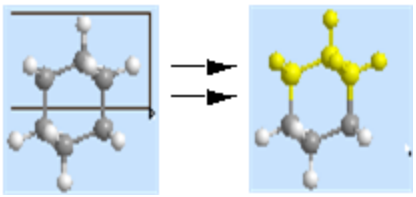
[1] Ionic compounds can consist of multiple fragments—one for each ion.

Note: *To select a bond, you can either click the bond or select both of its adjacent atoms.*

To select more than one atom, hold down either the SHIFT or CTRL key while selecting the atoms. To select all atoms and bonds in a model, go to **Edit**>**Select All** or type CTRL+A.
The model explorer provides an alternate way of selecting atoms and bonds. See "Model Explorer" on page 51.

Selecting ungrouped atoms

To select several atoms and bonds, click and drag across them with either the Move Objects tool, or Select tool, .



Atoms that are least partially within the selection rectangle are selected when you release the mouse button. A bond is selected only if both adjacent atoms are also selected.

Tip: *To select atoms one at a time or to add individual atoms to a selection, SHIFT-click each atom to add.*

Deselecting atoms and bonds

When you deselect an atom, you deselect all adjacent bonds. When you deselect a bond, you deselect the atoms on either end if the atoms are not connected to another selected bond.

- SHIFT+click an atom or bond to deselect it.
- Click an empty area of the Model window to deselect all atoms and bonds.

Changing elements

To change an atom from one element to another:

1. Click the Build from Text tool.
2. Click the atom to change. A text box appears.
3. Type the symbol for the element you want (case-sensitive).
4. Press ENTER.
5. (Optional) To apply the symbol again, double-click another atom.

Example
To change benzene to aniline:

1. Click the hydrogen atom to replace and type NH2.
2. Press ENTER.

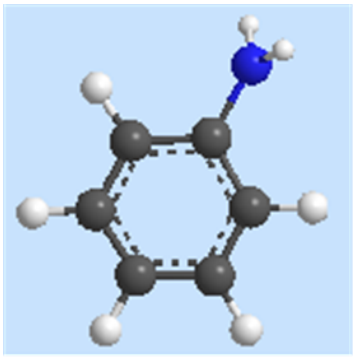


Figure 3.3: aniline model.

Kukele and delocalized bonds

Alternate double and single bonds in aromatics and other compounds can be displayed in either their Kekule or delocalized form. Two typical examples, CO_2^- and benzene, appear below.

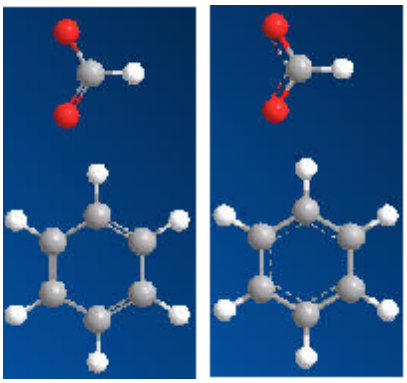


Figure 3.4: Kekule and delocalized bonds

After building your model, you can toggle between Kekule and delocalized bonds in any of three ways:

- In the model window, type CTRL+K.
- Go to **View**>**Model Display**>**Delocalized Bonds** and select an option.
- Go to **File**>**Model Settings**>**Model Display** tab and select (or deselect) **Show Delocalized Bonds as Dashed Lines**.

Setting selection color

Selected atoms and bonds are highlighted in yellow color by default. You can change the default selection color in the Model Settings dialog box.

1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. Click the **Color & Fonts** tab.
3. Select the desired color from the **Selection Color** drop-down list.

4. Click **OK**.

Adjusting bond width

You can adjust the width of some or all bonds in your model.
To adjust the width of one or more selected bonds:

1. Select one or more bonds.
2. Right-click the selected bond(s).
3. Choose **Select Object Bond Size** from the context menu. The bond size slider appears.
4. Move the slider to adjust the width.
5. (Optional) To reset the bond to its default width, right-click the bond and select **Reset to Default**.

To adjust the width for all bonds in your model:

1. Go to **File**>**Model Settings** and select the **Atom & Bond** tab.
2. Move the **Bond Size** slider to the desired width.
3. Click **OK**.
4. (Optional) To reset all bonds to their default width, go to **File**>**Model Settings**. Then, select the **Atom & Bond** tab and click **Reset to Default**.

Removing bonds and atoms

To remove an atom or bond:

1. Do one of the following to remove an atom or bond:

- Click the Eraser tool and click the atom or bond.
- Select the atom or bond, and go to **Edit** > **Clear**.
- Select the atom or bond and press DELETE.

Alternatively, to remove a bond, right-click the bond and select **Break Bond**.

Note: *If automatic rectification is on, you will not be able to delete hydrogen atoms. Turn automatic rectification off when modifying a model. (Go to* ***File****>****Model Settings****>****Model Building*** *tab.)*

Atom charges

Atoms are assigned a formal charge based on the atom type and bonding for that atom. You can display the charge by pointing to the atom.

Setting charges

To set the formal charge of an atom:

1. Click the Build from Text tool.
2. Select the atom(s) to change.
3. Type + or- followed by the number of the formal charge.

4. Press ENTER.

To set the formal charge of an atom in a molecular fragment as you build you, add the charge after the element in the text.

Example
To build a model of a phenoxide fragment:

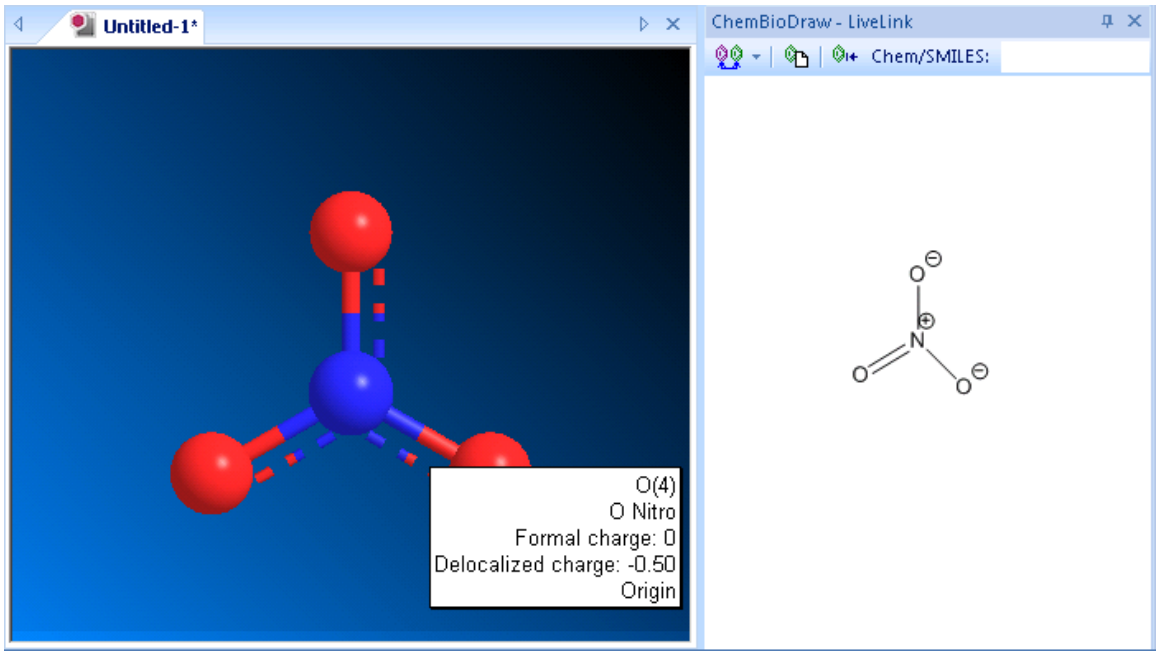
1. Type PhO- into a text box with no atoms selected.
2. Press ENTER. The phenoxide ion molecule appears.

To remove the formal charge from an atom:

1. Click the Build from Text tool.
2. Select the charged atom.
3. Type +0.
4. Press ENTER.

Displaying charges

ChemBio3D 13.0 recognizes formal and delocalized charges on atoms. As also shown in ChemDraw drawings, ChemBio3D 13.0 displays the formal charge that has been assigned to atoms and calculates the delocalized charge. If an atom possess a delocalized charge that is different from the formal charge, both charges are shown; otherwise, only the formal charge is displayed.



Object position

The position of every object in a model is defined by two sets of Cartesian coordinate axes—the model axes and the view axes. The model axes (green) determine the *absolute* position of all objects. An object does not change its position in relation to the model axes unless you move it.
The view axes (purple) define the *relative* position of all objects in the model. The view axes origin is the center of all objects in the model. As a result, all objects in the model move relative to the view axes origin whenever an object is added, deleted, or moved in the model window.

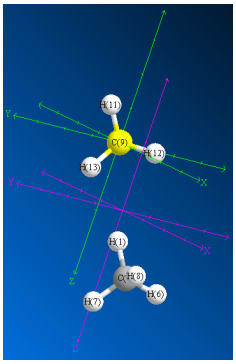


Figure 3.5: A model showing both sets of coordinates. The C(9) carbon is positioned at the origin of the model axes. All objects in the model (the two methane fragments) are centered around the origin of the view axes.

Moving objects

When you move an object, you change its position in relation to the model axes. For more information, see "Object position" on page 23.

1. Select the Move Objects tool in the Building toolbar.
2. Select one or more objects (to select multiple objects, SHIFT+ click each one).
3. Click-drag one of the selected objects.

When you move an atom, attached rectification atoms (typically hydrogens) move with it. When you move a bond, its adjacent atoms also move.

You can also use the Translate tool to move objects:

1. Select one or more objects in the model window.
2. While pressing SHIFT, click-drag the selected object(s) using the translate tool.

Centering a selection

When resizing a model or before performing computations, it is often useful to center the model.
ChemBio3D lets you select an atom (or atoms) to determine the center, or perform the calculation on the entire model.
To center your model based on a selection:

1. (Optional) Select one or more atoms.

2. Go to **Structure**>**Model Position**>**Center Model** (or **Selection**) **on Origin.**

This command places the centroid of the selected atoms at the origin of the model axes. ChemBio3D calculates the centroid of the selected atoms by averaging their X-, Y-, and Z-coordinates. If you do not select any atoms, the whole model becomes centered.

Substructures

A substructure is simply part of a structure (basically, a building block) that you can define and use to quickly build models. Substructures have attachment points to which other atoms or substructures connect. Several predefined substructures are listed in the substructures table (substructures.xml file). You can define your own substructures and add them to the table. See "Defining substructures" on page 24.

To apply a subtructure to a model, you can either add it to an existing fragment by replacing one of the fragment's atoms with the substructure or you can paste the subtructure into the model window as a new fragment.

To apply a subtructure to a model:

1. Go to **View**>**Parameter Tables**>**Substructures**.
2. In the substructures table, right-click the **Name** of a substructure and select **Copy**.
3. In your model, do one of the following:
   - To add the substructure to an existing fragment, right-click an atom in the fragment and select **Paste**.
   - To add the substructure as a new fragment, right-click an empty area of the model window and select **Paste**.

Defining substructures

To select a substructure:

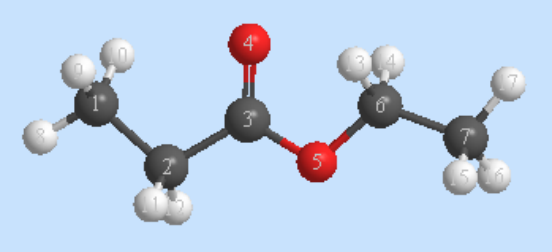
1. Build a model. Part (or all) of the model must include the atoms you want to define as the substructure. You can use ChemBio3D 13.0 tools or build it in the ChemDraw panel.
2. In the model, select the part (or all) of the structure you want to define as the substructure.
3. Go to **Edit**>**Copy**.

To save the substructure definition:

1. Go to **View**>**Parameter Tables**>**Substructures**. to open the substructures window.
2. Right-click in the Substructures table and choose **Append Row**. A new row is added to the table.
3. Select the cell in the **Model** column.
4. Right-click in the cell and choose **Paste** from the context menu. The content will be not be visible until you move to another cell.
5. Select the cell in the **Name** column.
6. Type a name for the substructure.
7. Close and save the Substructures table.

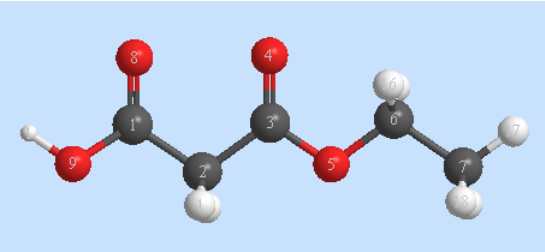
An example

Consider an ester substructure, R_1COOR_2. You can build this substructure as part of the model below:



Select atoms 3-5 (the two oxygen atoms and the carbon atom between them) and using the instructions above, create a new record in the Substructures table.

To append an ester onto the end of the chain as a carboxylic acid, double-click a hydrogen to replace it with the ester (as long as the name of the substructure is in the text box). Replacing H(8) (of the original structure) would produce this structure:



Notice that the carbon atom in the ester has replaced the hydrogen. This is because, when the ester was defined, the carbon atom had a lower serial number (3) than the oxygen atom that formed the other attachment point in the substructure (5).

Note: *When defining substructures with multiple attachment points, note the serial numbers of the atoms in the substructure so that you can correctly orient the substructure when it is inserted in the model. For more information, see* *"Attachment point rules" on page 26**.*

Advantages of using substructures

Here are some advantages for using substructures:

- Substructures may be energy minimized.
- Substructures have more than one attachment atom (bonding atom) pre-configured.

For example, the substructure Ph for the phenyl group has a single attachment point. The substructure COO for the carboxyl group has attachment points at the carboxyl carbon and the anionic oxygen. Similar multi-bonding sites are defined for all amino acid and other polymer units.

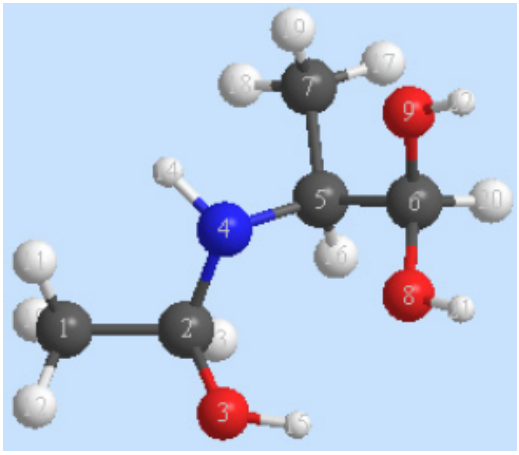
- Amino Acid substructures come in alpha and beta forms. If the name of the amino acid is preceded by the symbol ‘β‘ then it implies that the acid is in beta form, otherwise the acid is in alpha form. The dihedral angles have been preset for building alpha helix and beta sheet forms.
- You can use substructures alone or with single elements or atom types.

- Using a substructure creates a record in the Groups table that you can use for easy selection of groups, or coloring by group.
- Substructures are particularly useful for building polymers.
- You can define your own substructures and add them to the substructures table, or create additional tables. For more information, see "Defining substructures" on page 24.
- You must know where the attachment points are for each substructure to get meaningful structures using this method. Pre-defined substructures have attachment points as defined by standard chemistry conventions. For more information see "Attachment point rules" on page 26.

To use a substructure as an independent fragment, make sure no atoms are selected.
To insert a substructure into a model, select the atoms bonded to the substructure attachment points. To know how to use substructures to create models, see "Substructures" on page 74.

Angles and measurements

The measurements between the selected atoms and nearby unselected atoms are saved with the substructure. These measurements are used to position the substructure relative to other atoms when it is used in your model.
For example, ChemBio3D stores with the substructure a dihedral angle formed by two atoms in the substructure and two unselected atoms. If more than one dihedral angle can be composed from selected (substructure) and unselected (non-substructure) atoms, the dihedral angle that is saved with the substructure consists of the atoms with the lowest serial numbers.
Consider the following model to define a substructure for alanine:



Since polypeptides are specified beginning with the N-terminal amino acid, N(4) should have a lower serial number than the carboxyl C(6). To ensure that a chain of alanine substructures is formed correctly, C(1) should have a lower serial number than O(3) so that the C-C-N-C dihedral angle is used to position adjacent substructures within a label.

Attachment point rules

When you save a substructure, its attachment points are saved with it.

Attachment points follow these rules:

- If two atoms in the substructure are the same, the atom with the lowest serial number becomes the first attachment point.
- If an atom has an open valence and is attached to a selected atom, it is numbered after any atom that is attached to an unselected atom.
- If an atom is attached only to rectified atoms, it goes after any atom that is attached to non-rectification atoms.
- If two atoms are the same according to the above criteria, then the one attached to the atom with the lowest serial number goes first.

Refining models

After building a 3D model, you may need to make further refinements to help ensure that it is geometrically and structurally correct. For example, bond angles and lengths may not be chemically accurate if you've moved objects around or deleted them while building your model. You may also need to rectify atoms in your model to adjust their valences in cases where you may have deleted other atoms.

Rectifying atoms

When you rectify atoms in your model, hydrogen atoms are added and deleted as necessary so that each selected atom is bonded to the correct number of atoms. The correct number is specified by the valency of the atom type. The rectify command assigns atom types before rectification.
The atom types of the selected atoms are changed so that they are consistent with the bound-to orders and bound-to types of adjacent atoms.
To rectify selected atoms in your model:

1. Select the atoms to rectify.
2. Go to **Structure**>**Rectify.**

To set rectification as a default:

1. Go to **File**>**Model Settings** and select the **Model Building** tab.
2. Select **Rectify**.
3. Click **OK**.

Note: *The rectification setting does not affect fragments that already appear in the model window. To rectify existing atoms, select the atoms and go to* ***Structure***>***Rectify****.*

When **Correct Building Type** and **Rectify** settings are selected in the Model Building tab panel, the atom type is set according to the bond tool used and the appropriate number of hydrogens are added.

Rectifying atoms in PDB files

While opening a PDB file, you can specify that the hydrogens in the PDB file model be rectified.
To add hydrogens to PDB file:

1. Go to **File>Open**.

2. Select a PDB file to open.
3. Select the following check boxes:
   - Compute Atom Types and Bond Orders
   - Rectify Atoms
4. Click **Open**.

Upon import, hydrogens will be added to the molecule from the PDB file.

Cleaning up a model

As you build your model or arbitrarily move objects around the model window, your model may begin to appear distorted. To correct the distortion, use the **Clean Up** command. To clean up the selected atoms in a model:

1. Select a part or all of the model to clean up.
2. Go to **Structure**>**Clean Up**.

When you use the clean up command, the selected atoms are repositioned to reduce errors in bond lengths and bond angles. Planar atoms are flattened and dihedral angles around double bonds are rotated to 0 or 180 degrees.
Also, any bond lengths or bond angles you may have set in the measurements table are overridden. ChemBio3D tries to adjust the structure so that its measurements match those in the **Optimal** column. These optimal values are the standard measurements in the Bond Stretching and Angle Bending parameter tables. For all other measurements, performing a Clean Up or MM2 computation alters these values. To use values you set in these computations, you must apply a constraint. See "Setting constraints" on page 79 for information.

Copying and printing

ChemBio3D offers several options for you to copy, embed, and print models. The best option depends on your needs and preferences.

Copying

You can copy ChemBio3D models into other applications such as a desktop publishing program. How you copy the model depends how you want the model to appear in the new application.
When you copy a model from ChemBio3D into another application, the model retains its properties. If you want to edit the model, you can only do it using ChemBio3D. After you edit and save the structure, the changes will be reflected in the application where you have pasted the model.

Copying as an editable model

To copy a model:

1. In ChemBio3D, select the model.
2. Go to **Edit**>**Copy**.

3. In the other software application, paste the model into an open file. For example, in Microsoft® Word, type **CTRL+V**.

After you paste the model into the application, you can edit it when needed.
To edit a pasted model:

1. In the application in which the model is pasted, double-click the model image. The model opens in ChemBio3D.
2. In ChemBio3D, edit the model.
3. In ChemBio3D, go to **File**>**Exit & Return**. ChemBio3D closes.

Copying as a static image
You can copy a model as either a bitmap or enhanced meta file (EMF). Bitmap files retain the background you see in ChemBio3D while the EMF adopts the background (typically white) used in the application in which it is pasted.

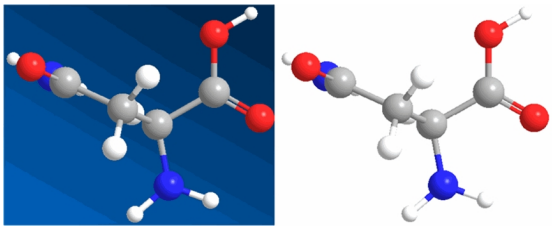


Figure 3.1: A model of asparagine imported as a bitmap (left) and as an EMF (right).

When pasted into other applications, these files become static images and cannot be modified. However, bitmap and EMF files typically have a smaller file size than embedded models.
To copy and paste a model as a static image:

1. Select the model.
2. Go to **Edit**>**Copy As** and choose either **Bitmap** or **Enhanced Metafile**.
3. In the other software application, paste the model into an open file. For example, in Microsoft® Word, type CTRL+V.

When you copy in a graphic format, the size of the model window determines the size of the file that you copy to the clipboard from ChemBio3D. To adjust the size of a copied molecule, resize the model window before you copy it.

Tip: *To export copies of several models so that they are all the same size, adjust the model windows so that they are the same size and ensure that Fit Model to Window is on. To turn on the Fit Model to Window feature, go to* ***File > Model Settings > Model Building*** *tab and select the Fit Model to Window check box.*

Copying to ChemBioDraw
Models that you copy to ChemBioDraw appear as 2D drawings. This means that you can edit a drawing as you would any other ChemBioDraw structure.
To copy a model into ChemBioDraw:

1. Select the model.

2. Go to **Edit**>**Copy As**>**ChemDraw Structure**.
3. In ChemBioDraw, go to **Edit**>**Paste**.

Copying as simple notation

To copy the model as a SMILES, InChI, or InChIKey string, select the model and go to **Edit**>**Copy As** and choose either **SMILES**, **InChI**, or **InChIKey**.

Embedding

The ChemBio3D 13.0 ActiveX control lets you embed models in Microsoft PowerPoint, Word, HTML-based documents, or any COM-aware application.

Note: *To see an embedded object of ChemBio3D in Microsoft Word, you may need adjust the macro security settings. The macro security settings should be either Low or Medium with macros enabled.*

When a model is embedded, you can view it using many of the features found in ChemBio3D. For example, you can rotate the model, zoom in and out, and change its display mode.

To embed a model:

1. In ChemBio3D, type CTRL+A to select the model.
2. Go to **Edit**>**Copy As**>**Embedded Object**.
3. Launch the other application (such as PowerPoint).
4. To paste the object in the target document, type CTRL+V.

Note: *To view an embedded model in PowerPoint, go to PowerPoint and press F5 to begin the slide show.*

Figure 3.2: A ChemBio3D model embedded in FrontPage.

Note: *Modifying the embedded image in HTML is beyond the scope of this document. If you are a programmer developing 3D modeling HTML pages, see ReadMeC3DP.htm in the ChemBio3D application folder.*

When you embed a model in a PowerPoint presentation, you can modify the display properties. Select **Properties** from the context (right-click) menu.

Listed below are the properties you can change in an embedded object.

AutoRedraw. By default, this is set to True.
DemoAxis. Defines the axis of rotation when you select DemoRock or DemoSpin as a DemoMode.
DemoMode. Determines whether the model rocks, rotates or remains static in the slideshow.
DemoSpeed. The relative rotation speed when the DemoMode is set as either DemoRock or DemoSpin.
EncodeData. Cannot be changed. By default, this is set to True.
Fullscreen. Cannot be changed. By default, this is set to False.
Height. Defines the height of the object window.
Left. Defines the placement of the left edge of the object window.
Modified. Cannot be changed.
Rock amplitude. The amplitude in which the model will rock when the DemoMode is set to DemoRock.
ShowContextMenu. Shows/hides right-click menus in the object window.
ShowRotationBar. Shows/hides the Rotation toolbar.
ShowToolbar. Determines placement of the Toolbar (left, right, top, bottom) or hides the toolbar.
Top. Defines the top of the object window, measured from the top of the slide.
ViewOnly. Set to False by default.
Visible. Shows/hides the object window.
Width. Defines the width of the object window.

Printing

You can print your models to either an Adobe PostScript or non-PostScript printer.
When you print your model, you can specify several options, such as the image scale and resolution.
To set print options:

1. Go to **File**>**Print Setup**. The Print Setup dialog box opens.
2. In the **Printer** drop-down list, select a printer.
3. In the **Form** drop-down list, select the size of the paper.
4. Select an orientation.
5. Select from these options:

Scale To Full Page. The model size is adjusted to the page size.
Scale to____ mm/Angstrom.
Always print with White Background. White will replace the background color that appears on the screen.
High resolution Printing. Select for higher quality. Deselect for faster printing.
Include a Footer. A footer appears on the printed page.

6. Click **OK**.

To print:

1. Go to **File**>**Print**. The Print dialog box opens.
2. Click **OK**.

Finding structures online

ChemBio3D includes online resources from which you can download structures and view them in the model window. For example, you can download files from the Protein Data Bank (PDB), Crystallographic Information File (CIF), or Available Chemicals Exchange (ACX) databases. To download a PDB or CIF file, you will need either its PDB or CIF number. To download an ACX file, you will need either its ACX number or the structure name.

Caution: *If the ChemDraw panel is open while you are downloading large structures, you may receive an error message: "The number of atoms in this molecule exceeds the atom synchronization limit. The ChemDraw panel cannot load the molecular structure." Close the error message. The downloaded structure will appear in the model window but not in the ChemDraw panel.*

PDB and CIF files

To download either a PDB or CIF file:

1. Go to **Online**>**Find Structure from PDB ID**. A dialog box opens.
2. In the dialog box, either enter the PDB ID for the structure in the **PDB ID** drop-down list or select it from the list.
3. In the **Format** drop-down list, select either PDB or CIF.
4. To enter a location to save the file, select **Save As** to navigate to the save location.
5. Click **Get File**. The file is downloaded and appears in a new model window.

ACX files

To download an ACX file using its ACX number:

1. Go to **Online**>**Find Structure from ACX Number**. A dialog box opens.
2. In the dialog box, either enter the ACX number for the structure in the **ACX No** drop-down list or select it from the list.
3. To enter a location to save the file, select **Save As** to navigate to the save location.
4. Click **Get File**. The file is downloaded and appears in a new model window.

To download an ACX file using a structure name:

1. Go to **Online**>**Find Structure from Name at ChemACX.com**. A dialog box opens.
2. In the dialog box, either enter the structure name in the **Name** drop-down list or select it from the list.
3. To enter a location to save the file, select **Save As** to navigate to the save location.
4. Click **Get File**. The file is downloaded and appears in a new model window.

Ordering from ChemACX

You can order chemicals through ChemACX from the ChemBio3D main menu.

Note: *To order chemicals, you must have the ChemDraw ActiveX control installed.*

To order a chemical:

1. With a model in the model window, go to **Online**>**Find Suppliers on ChemACX.com**.

2. Install the ChemDraw ActiveX control if prompted.

Note: *You should be registered and /or logged in to the PerkinElmer Web site before proceeding with the following steps.*

3. The ChemACX Database Web site opens in a browser window with the structure displayed.
4. In the **Suppliers list**, select a supplier from whom to order. A list of products from the selected supplier appears.
5. In the product list, select one or more products to order and click **Add to Cart**.
6. When you are ready, click **View Shopping Cart** and complete your order.

Note: *For information on how to order chemicals using ChemACX, click* ***Help*** *in the ChemACX main menu.*

Displaying Models

The display options in ChemBio3D not only let you add visual appeal to models but are also designed to help you examine structural properties. Using basic tools, you can scale, rotate, and move various objects in your model. You can also add color to identify objects or show atomic distance and bond angle measurements.

Display modes

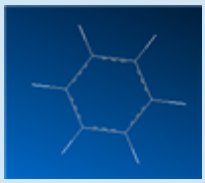
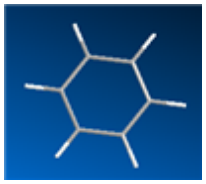
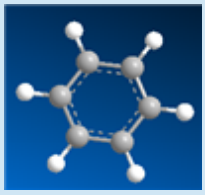
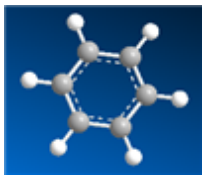
Display modes define how bonds and atoms appear. Models appear in the Ball & Stick display mode by default. To change the display mode, go to **View**>**Model Display**>**Display Mode** and select a display mode option. You can also change the display mode for model fragments. See "Display modes for fragments" on page 57. The display modes are described below.

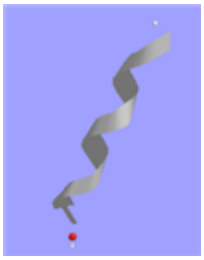
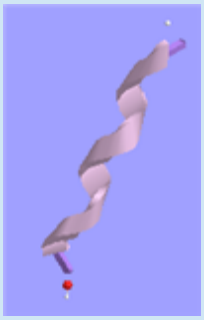
Setting the default display mode

ChemBio3D applies the default display mode whenever you open a new model window.
To set the default display mode:

1. Go to **File**>**Model Settings**. The **Model Settings** dialog box appears.
2. Select the **Model Display** tab.
3. Select an option in the **Model Type** drop-down list.
4. Click **Set as Default**.
5. Click **OK**.

The table below describes the display modes:

Display Mode	Description
Wire Frame 	Wire frame is the most simple display mode. Bonds are displayed as pixel-wide lines. Atoms are not displayed explicitly, but each half of a bond is colored to represent the element color for the atom. Wire frame models are well suited for extremely large models such as proteins.
Sticks 	Stick models are similar to wire frame, however, the bonds are slightly thicker. This model type is also good for visualizing very large models such as proteins.
Ball and Stick 	These models show bonds as thick lines and atoms as filled spheres. The atom spheres are filled with color that corresponds to the element or position of the atom.
Cylindrical Bonds 	These models are similar to Ball and Stick models except that all bond types are drawn as cylinders.
Space Filling	These models are best for getting an idea about the relative physical size of the atoms. Each atom's size is determined by its van der Waal's (VDW) radius. These models may be complex to draw and slow to display. Atoms are scaled to 100% of the van der Waals radii specified in the Atom Types table. The van der Waal's radii may be set so that overlap between non-bonded atoms indicates a large (about 0.5 kcal/mole) repulsive interaction.
Ribbons	These models show large protein molecules in a form that highlights

Display Mode	Description
	secondary and tertiary structure. Ribbon models can be colored by group to identify the amino acid constituents. Your model must have a protein backbone to display ribbons.
Cartoons 	Cartoon models, like ribbon models, show large protein molecules in a form that highlights secondary and tertiary structure. Ribbon and Cartoon model display modes do not provide pop-up information and are not intended for printing as bitmaps.

Atom and bond size

You can adjust the size of atoms and bonds in ball and stick, cylindrical bonds, and space filling models.

1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. Select the **Atom & Bond** tab.
3. To view your changes before you apply them, select **Preview**.
4. To adjust the atom size, move the **Atom Size** slider.
5. To adjust the bond size, move the **Bond Size** slider.
6. Click **OK**.

The Atom Size value, 0 (small) to 100 (large), is a percentage of the covalent radius specified for each atom in the Elements table. When the Atom Size is 100, the atoms are scaled to their maximum radii. The value of this setting affects Ball and Stick and Cylindrical Bond models.

📝 ***Note:*** *To open the Elements table, go to* ***View***>***Parameter Tables***>***Elements***.

Displaying dot surfaces

You can add dot surfaces to any of the model display modes. Go to **View**>**Model Display**>**Show Atom Dots**. An example using a stick model is shown below.

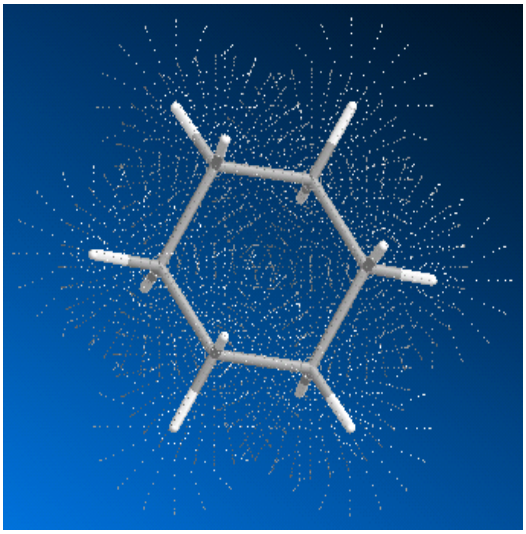


Figure 4.1: Viewing dot surfaces.

To show atom dots for only selected atoms:

1. In the model window, select one or more atoms.
2. Right-click one of the selected atoms.
3. In the context menu, go to **Atom Dots**>**Show Atom Dots**.

To display dot surfaces by default on all atoms:

1. Go to **File**>**Model Settings** and select the **Atom & Bond** tab.
2. In the **Atom Dot Surfaces** section, click the **Show by Default** check box.
3. Use the **Density** slider to adjust the density of the dot surface and click **Apply**.
4. Click **OK**.

Serial numbers

Each atom in a model is assigned a unique serial number to distinguish it from all other atoms. As a result, you can identify each atom when viewing the model explorer or measurements table.
To view the serial numbers, select one of these options:

- For individual atoms, use the Select tool to point to the atom. The serial number appears in the pop-up information.
- Go to **View**>**Model Display**>**Show Serial Numbers**. Serial numbers for all atoms are displayed.
- Go to **File**>**Model Settings**>**Model Display** tab and check the **Show Serial Numbers** check box. Click **Apply** and then click **OK**.
- Click the Serial Number toggle on the Model Display Toolbar.

Reassigning serial numbers

Serial numbers are initially assigned based on the order in which you add atoms to your model.

To reassign the serial number of an atom:

1. In the model explorer, select the atoms to renumber.
2. Right-click the selected atoms and go to **Atom Serial Numbers**>**Hide Atom Serial Numbers.**

Note: *The model explorer cannot update its numbering to match the changes you are making on the model when Serial Numbers are displayed. If you forget this step, you will see different numbers on the tree control and the model. If this happens, hide the serial numbers momentarily and display them again.*

3. Click the Build from Text tool.
4. Click the atom you want to reserialize. The atom is selected and a text box appears.
5. Type the serial number.
6. Press ENTER.
7. Right-click the atom that you reserialized and go to **Atom Serial Numbers**>**Show Atom Serial Numbers.** The new serial number of the atom appears.
8. Repeat step 4 to step 7 for all the atoms that you want to reserialize.

If the serial numbers of any unselected atoms conflict with the new serial numbers, then those unselected atoms are also reserialized.

To reserialize another atom with the next sequential number, double-click the next atom you want to reserialize.

To reserialize several atoms at once:

1. Click the Build from Text tool.
2. Hold down SHIFT and select several atoms.
3. Type the starting serial number.
4. Press ENTER.

Normally, the selected atoms are reserialized in the order of their current serial numbers. However, the first four atoms selected are reserialized in the order you selected them.

Displaying atoms

Using the model explorer, you can control which atoms are displayed in the Model Window.

To hide atoms or groups, right-click at any level, point to **Visibility** and click **Hide**... (Atom Group, etc.). Hidden atoms or groups are displayed in parentheses in the tree control.

By default, all levels in the hierarchy are set to inherit the settings of the level above, but you can reset the default to hide a group but show individual atoms in it.

Showing atoms

To show an atom in a hidden group, right-click the atom in the model explorer, point to **Visibility** and click **Show**.

Showing all atoms

If you are working with a large model, it may be difficult to keep track of everything you have hidden. To show all atoms or groups that are hidden:

1. Select a level in the tree control above the hidden atoms or groups, or SHIFT+click to select the entire model.
2. From the context menu point to **Select** and click **Select All Children**.
3. Right-click again, point to **Show** and choose **Inherit Setting**.

Atom symbols

You can display symbols on the atoms in your model to explicitly show the elements they represent.

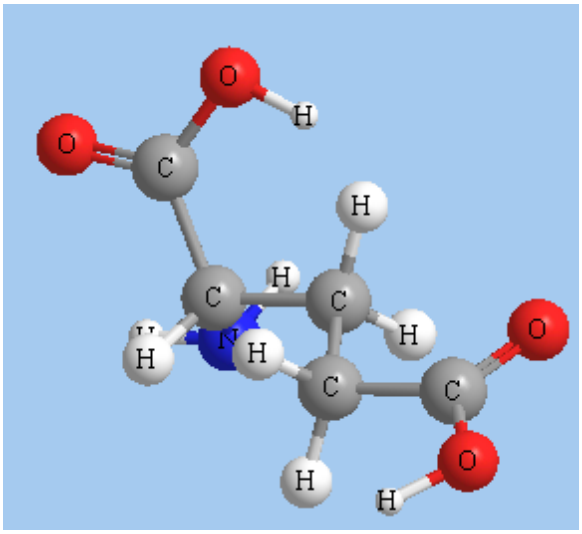


Figure 4.2: Glutamic acid with atom symbols displayed.

To display symbols for all atoms, do one of the following:

- Go to **View**>**Model Display**>**Show Atom Symbols.**
- Click the Atom Symbol icon on the Model Display toolbar.
- Right-click an empty area of the model window and select **Show Atom Symbols** in the context menu.

To display symbols for selected atoms:

1. Select the atoms in the model window.

Tip: *You can also select the atoms in the model explorer. Either SHIFT+click or CTRL+click the atoms from the list.*

---

2. Right-click one of the selected atoms. A context menu appears.
3. Go to **Atom Symbols**>**Show Atom Symbols**.

To set the appearance of atom symbols to their defaults:

1. Go to **File**>**Model Settings**.
2. On the **Colors & Fonts** tab, select the atom label font, point size, and color.
3. Click **Set as Default**. All atoms currently in the model window display the selected options.
4. Click **OK**.

Note: *The default appearance setting also affects the serial number.*

Rotating models

By default, when you rotate a model, all objects in the model window rotate together. However, ChemBio3D provides many options for rotating objects. You can rotate each fragment (or part of a fragment), rotate objects around axes, a specified bond, or a dihedral bond.

Free rotations

You can freely rotate your entire model to any angle around any axis.
To freely rotate a model:

1. Select the Rotate ( ) tool.
2. Click-drag anywhere in the model window.

The Status bar displays the X- and Y-axes of rotation.

Rotating a fragment

You can also rotate one or more fragments that you select.
To rotate one or more fragments:

1. Select an atom in each fragment you want to rotate.
2. Select the rotation tool, hold the SHIFT key and click-drag anywhere in the model window.

Axis rotations

You can rotate your model around the X-, Y-, and Z-axes. These axes are defined by the model window. The horizontal and vertical axes of the window define the X- and Y-axes of rotation; the Z-axis is perpendicular to the window. These axes are independent of the view and model axes. (For more on the view and model axes, see "Object position" on page 23).

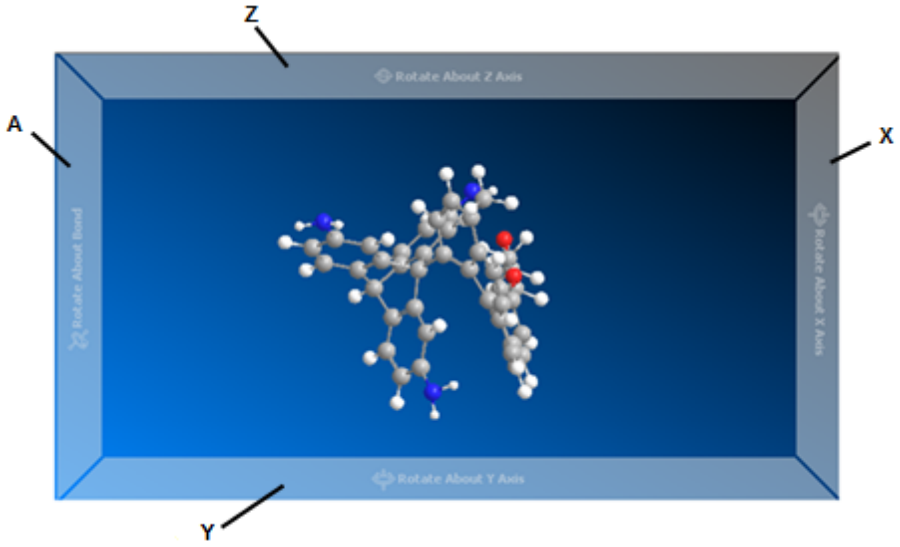


Figure 4.3: The rotation bars. A) Bond rotation bar; X) X-axis rotation bar; Y) Y-axis rotation bar; Z) Z-axis rotation bar.

To rotate a model around either the X-, Y-, or Z-axis:

1. (optional) Go to **View**>**Model Display**>**Model Axes** to display the view axes.
2. Select the Rotate ( ) tool.
3. Point to an edge of the model window, the rotation bars appear.
4. Click-drag the pointer around the rotation bar for the axis you want to rotate the model around.

The angle of rotation appears in the Status bar.

Hiding rotation bars

By default, the rotation bars appear whenever you use them. However, you can always keep them hidden even when you are using them.

To hide/display the rotation bars:

1. Go to **File**>**Preferences** and select the **GUI** tab.
2. To show/hide the rotation bars select/deselect **Show Mouse Rotation Zones.**
3. Click **Apply** and then click **OK**.

Note: *The rotation bars are active when you select the Rotate tool, even if they are hidden.*

Rotating around a bond

To rotate the model around a bond:

1. Select the bond using the Select tool.
2. Using the Rotate tool, drag the mouse along the **Rotate About Bond** Rotation bar on the left side of the Model window.

The rotation dial

The rotation dial lets you specify an angle of rotation around a bond or a dihedral to create another conformation of your model.

To open the rotation dial, click the arrow next to the Rotate tool.

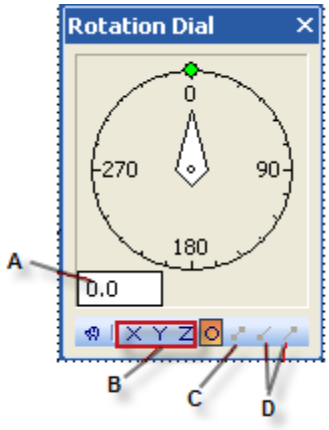


Figure 4.4: The Rotation dial: A) degree display box; B) Axis rotation; C) Local (rotate around bond) axis; D) dihedral rotation.

Rotating around a dihedral

To rotate around a dihedral:

1. Select either two or four adjacent atoms.
2. In the rotation dial, select one of the dihedral rotation options.
3. In the rotation dial, either enter a value in the degrees display box or click-drag the dial to the desired angle.

Tip: *Use the keyboard shortcuts SHIFT+B and SHIFT+N to control which part of the model moves in the dihedral rotation.*

You can change the orientation of your model along a specific axis. Although your model moves, the origin of the model (0, 0, 0) does not change, and is always located in the center of the model window. To change the origin, see "Centering a selection" on page 23.

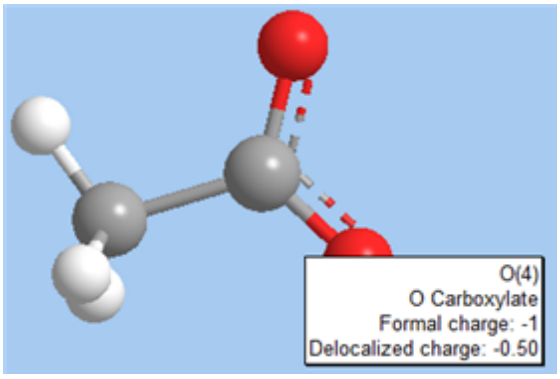
Rotating around a bond

To rotate around a bond:

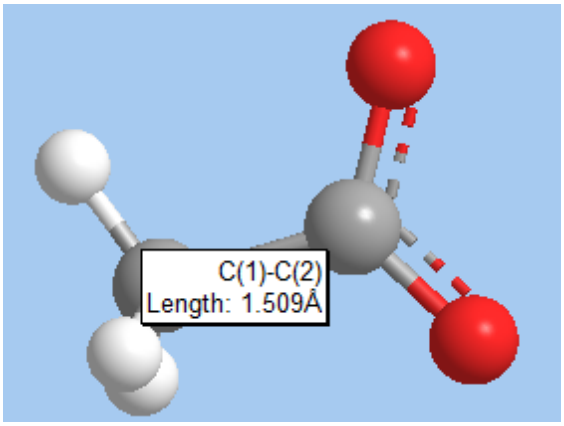
1. Select either two adjacent atoms or a bond.
2. In the rotation dial, select the Local Axis option.
3. In the rotation dial, either enter a value in the degrees display box or click-drag the dial to the desired angle.

Atom and bond properties

When you point to an atom or bond, its properties appear in a pop-up window.
Here is an example for an atom:



This example is for a bond:



The properties begin with the atom label, such as C(1) for an atom or C(1)-C(2) for a bond. To choose other information you want to appear, go to **File**>**Preferences** and select the **Popup Info.** tab.
The options are described below:
Cartesian Coordinates. Displays the three numerical values indicating the atom's position along the X, Y, and Z-axes.
Atom Type. Displays the atom type corresponding to the first column of a record in the Atom Types table.
Internal coordinates. Lists the relative positions and angles of atoms in the model relative to the origin atom.
Measurements. Displays the distance between two selected atoms, the angle formed by three selected atoms, or the dihedral angle formed by four selected atoms.
Bond Length. Displays the distance in angstroms between the atoms attached by a bond.
Bond Order. Displays the bond orders calculated by Minimize Energy, Steric Energy, or Molecular Dynamics.

Bond orders are usually Single, Double, or Triple depending on whether the bond is a single, double, or triple bond. Computed bond orders can be fractional.

Note: *Precise bond orders for delocalized pi systems are displayed if the MM2 Force Field has been calculated.*

Partial Charge. Displays the partial charge according to the currently selected calculation.
See "Surface types" on page 62 for information on how to select a calculation.
Group Name. Displays the group name if the selected atom is part of a group.
Show MM2 Bond Order Instead of ChemBio3D Bond Order. Displays the bond order based on MM2 calculations.
Show Customized Atom Properties. Shows properties that are listed in the columns of the Atom Property table. To view the Atom Property table, go to **View > Atom Property Table**. The columns are populated by a variety of methods (e.g. running an MM2 minimization)

Showing hydrogen bonds

ChemBio3D 13.0 can detect and display hydrogen bonds and polar hydrogen atoms. ChemBio3D recognizes these hydrogen bond donor and acceptor groups:
Hydrogen bond donors:

- *-N-H
- *-O-H

Hydrogen bond acceptors:

- Oxygen atoms with at least one available lone pair
- Nitrogen atoms with at least one available lone pair

To display hydrogen bonds, do one of the following:

- Go to **View**>**Model Display**>**Show Hydrogen Bonds** and choose either **Show Intermolecular** or **Show All**.
- Go to **File**>**Model Settings** and select the **Model Display** tab. From the **Hydrogen Bonds** drop-down list, select **Show intermolecular** or **Show All**.

Hydrogen bonds appear as dashed lines between the donor hydrogen and the acceptor atom. Bonds with less than ideal geometry are displayed with a blue tint. The color intensity increases as the bond becomes less ideal.

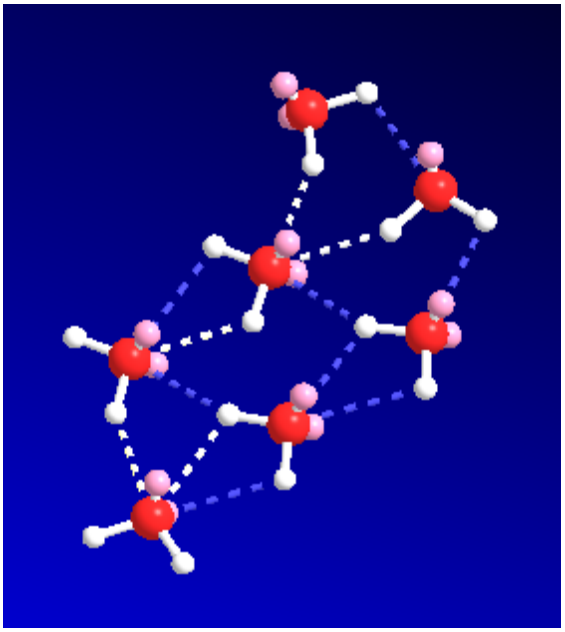


Figure 4.5: Hydrogen bonds in MM2 optimized water.

There are separate controls for hydrogen atoms and lone pairs, and you can choose to display only polar hydrogens (those bonded to oxygen or nitrogen).
To display hydrogen atoms and lone pairs:

1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. Click the **Model Display** tab.
3. Select **Show All** from the **Hydrogen Atoms** drop-down list.
4. Select **Show** from the **Lone Pairs** drop-down list.
5. Click **OK**.

By default, **Show Polar** is selected when a macromolecular PDB or mmCIF file is loaded.
These display modes are global options, but you can override their effect by changing the display mode of a particular atom or group in the model explorer.

Hydrogens and lone pairs

To show all hydrogen atoms or lone electron pairs in the model, go to **View**>**Model Display** and select either:

- **Show hydrogen atoms**>**Show All**.
- **Show Lone Pairs**>**Show All**.

Translating models

You can pan your view of the model vertically and horizontally using the translate tool. No objects in the window move; you just change the position from which you view the model (the effect is similar to using scroll bars in a Web browser).

To translate a model:

1. Select the Translate tool on the Building toolbar.
2. Click-drag anywhere in the model window.

You can also use the translate tool to move objects:

1. Select one or more objects in the model window.
2. While pressing SHIFT, click-drag the selected object(s) using the translate tool.

Scaling models

With the zoom tool selected, click and drag vertically in the model window to magnify or reduce the model size. The coordinates of the model do not change. You can also use the wheel if you are using a scrolling mouse.

You can scale a model to fit the window that contains it:

To scale a model to the window, go to **View**>**View Position**>**Fit to Window**.

Note: *The Fit command affects only the scale of the model. Atomic radii and interatomic distances do not change.*

Fit Model to Window

You can specify whether to resize and center the model in the model window whenever you make a change.

1. Go to **File**>**Model Settings**.
2. In the **Model Building** tab, select **Fit Model to Window** and click **OK**.

Aligning models

You can align a model either to an axis or to a plane.

Aligning to an axis

You can select any two atoms in a model and align them to either the X, Y, or Z-axis. The atoms don't have to be in the same structure.

1. To view the axes, select the Model Axes and View Axes buttons in the model display toolbar.
2. Select any two atoms.
3. Go to **Structure**>**Model Position**>**Align Model with** (X, Y, or Z) **Axis**.

The model becomes oriented so that the two atoms you select are parallel to the chosen axis.The command, **Align View (X, Y, or Z) Axis with Selection** align the axis joining the selected atoms parallel to the X, Y or Z axis, where the Z axis is orthogonal to the screen, the X axis runs from left-to-right and the Y axis runs down-to-up on the screen.

To orient the selected atoms with the screen:

4. Make sure the aligned atoms are still selected (or reselect them).
5. **Go to View>View Position>Align View** (X, Y, or Z**) Axis with Selection**.

For example, to see an end-on view of ethanol:

1. Click the Select tool.
2. SHIFT+click **C(1)** and **C(2)**.

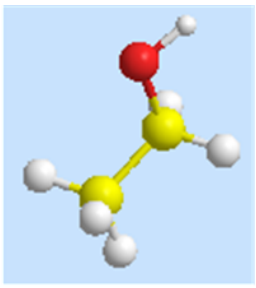
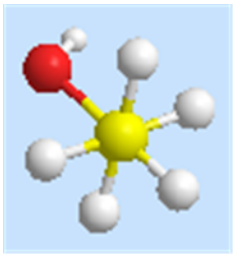


Figure 4.6: Selecting atom for alignment.

3. Go to **View**>**View Position**>**Align View Z Axis With Selection**.



Aligning to a plane

You can align your model to any Cartesian coordinate plane that you define. To align a model to a plane, you first select at least three atoms to define the plane. If you select more than three atoms, a plane is computed that minimizes the average distance between the selected atoms and the plane, commonly known as the best-fit plane.
To align the model to a plane:

1. Select three or more atoms.
2. Go to **Structure**>**Model Position**>**Align Model** (choose a plane) **With Selection**.

The model rotates so that the computed plane is parallel to the plane you choose (X-Y, Y-Z, or X-Z).
To move three atoms to a plane and two of the atoms onto an axis:

1. Select the two atoms.
2. Go to **View**>**View Position**>**Align View (**choose an axis**) With Selection**.
3. SHIFT+click the third atom.
4. Go to **View**>**View Position**>**Align View (**choose a plane) **With Selection**.

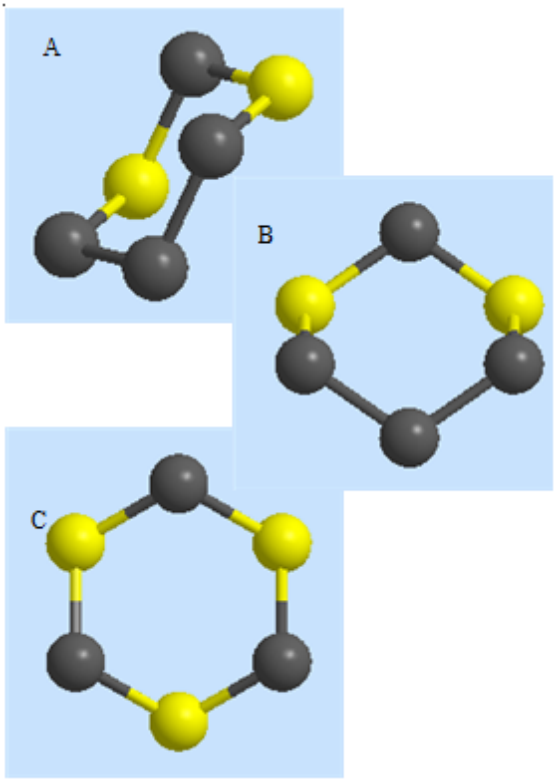
For example, to move a cyclohexane chair so that three alternating atoms are on the X-Y Plane:

1. Select two non-adjacent carbon atoms in the ring.
2. Go to **View**>**View Position**>**Align View X Axis With Selection**.

The model moves to the position shown in Figure B.

3. Select the third non-adjacent carbon atom in the ring.
4. Go to **View**>**View Position**>**Align View X-Y Plane With Selection**.

The model moves to the position shown in Figure C.

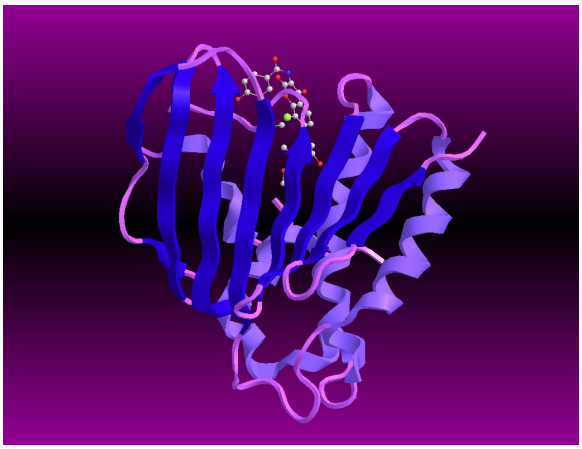


Applying color

Although you can use color to add visual appeal to a model, color can also be an important tool for identifying model fragments, functional groups, surfaces, and individual atoms.

Customizing the background

You can change the background color or replace the background with a picture (such as your company logo). A dark background is often suitable for ribbon displays intended for full color viewing, whereas a light background is useful for print.



To customize the background:

1. Go to **File**>**Model Settings** and select the **Background** tab.
2. Choose from these options:
   - To change the background color, select from the **Background Color** drop-down list.
   - To insert a picture, select **Background Picture** and choose from the **Transparency** and **Position** options to modify the picture.
   - To return to the default background, click **Reset to Default**.
3. Click **OK**.

Note: *The background colors are not saved in PostScript files or used when printing except when you use the ribbons display.*

Coloring selected atoms

To change the color of one or more atoms:

1. Select the atom(s).
2. Right-click an atom you selected and choose **Color**>**Select Color** in the context menu. The **Color** dialog box appears.
3. Select a color and click **OK**. The color of the atom(s) changes to the new color.

To remove a custom atom color from the model display:

1. Select the atoms whose colors you want to change.
2. Right-click the atoms you selected and go to **Color**>**Apply Object Color**>**Inherit Object Color**.

Coloring displays

There are two ways for you to set the colors used to display your model. You can set the colors either in the model settings or in the model display menu.

- To apply colors using the model settings, go to **File**>**Model Settings** and select the **Colors & Fonts** tab.
- To make a temporary change, go to **View**>**Model Display**>**Color By** and select a menu option.

You can color by:

- Monochrome--atoms and bonds are grayscale.
- Chain
- Element--atoms inherit the default color for the element they represent.
- Group--atoms inherit the color assign to the group to which they belong if the group has been assigned a color.
- Depth--atom color is determined by its relative position along the Z-axis.

📝 ***Note:*** *Monochrome and chain are available only for proteins displayed in the ribbon or cartoon display mode.*

Coloring by element

Color by element is the default mode for small molecules. The default colors are stored in the Elements table.

To change the color of elements specified in the Elements table:

1. Go to **View**>**Parameter Tables**>**Elements**. The Elements table opens.
2. Double-click the **Color** field for an element. The Color dialog box appears.
3. Select the color to use and click **OK**.
4. Close and save the table.

📝 ***Note:*** *You must save the changes for the new colors to take effect.*

Coloring by group

You can assign different colors to groups (substructures) in the model.

To change a color associated with a group in the active model:

1. In the model explorer, right-click on the group name and choose **Color>Select Color**. The Color dialog box appears.
2. Select the color to use and click **OK**.

Coloring by substructures

If the groups in your model are substructures defined in the Substructures table (substructures.xml), you can assign standard colors to them.

To assign (or change) a color:

1. Go to **View**>**Parameter Tables**>**Substructures**.
2. For the substructure whose color you want to change, double-click its corresponding cell in the Color column.The Color dialog box appears.
3. Select a color and click OK.
4. Close and save the Substructures table.

Once colors are assigned in the Substructures table, you can use them to apply color by group:

1. Go to **File**>**Model Settings**.
2. Select the **Colors & Fonts** tab.
3. Select **Group** in the **Color by** section. Each atom in your model appears in the color specified for its group.

📝 ***Note:*** *Color by Group is displayed only in ribbon and cartoon display modes.*

Coloring by partial charge

When coloring by partial charge, atoms with a highly negative partial charge are deep blue. Atoms with a highly positive partial charge are deep red. As the partial charge gets closer to 0, the color becomes pale. Atoms with a 0 partial charge are white.

The partial charge is the result of a calculation—Extended Hückel, CS MOPAC, or Gaussian. If you have not performed a calculation, the partial charge for each atom is 0.

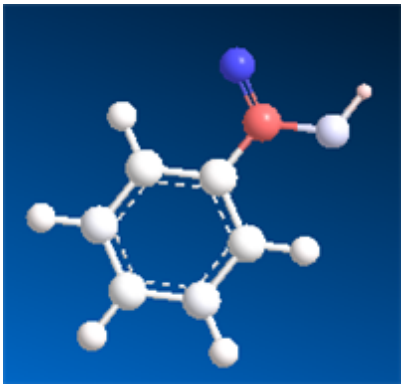


Figure 4.7: Color by partial charge.

Model Explorer

The model explorer provides you with an easy way to explore the structure of any model, even complex macromolecules, and alter display properties at any level. The model explorer lists all the structures in the model window, the atoms they contain, and any structural features (such as active sites in a protein) that you may have defined. To display the Model Explorer, Go to **View**>**Model Explorer**.

The display properties you can alter include:

- the display mode (ball & stick, wire frame, etc).
- visibility of each fragment.
- the color of the atoms in each fragment.

At the atom level, you can display or hide:

- atom spheres.
- atom dots.
- element symbols.
- serial numbers.

Model Explorer also lets you add and remove fragments into Structure Browser window.

Model Explorer objects

The model explorer displays all the objects in your model. If your model consists of more than one structure, each structure is defined as a fragment that has bonds and atoms as its child objects. Every object has a set of properties, including a property that defines whether or not it belongs to a parent object.
You can use the model explorer to group objects together and assign properties to them. Grouped objects do not have to be contiguous objects in your model or even be part of the same structure. For more information see Groups.

Note: *To display the Model Explorer, Go to* ***View>Model Explorer****.*

The default setting, all properties for an object, is inherited from its parent. This means that the parent determines the properties of its child objects until you change a property. By changing properties of a child object, you can visualize the part of the model you want to study.
You can use the model explorer to:

- Define objects.
- Add objects to groups.
- Rename objects.
- Delete objects with or without their contents.

Each type of object that can appear in the model explorer is described below:

Atoms
Each atom object in the model explorer represents one atom in your model. Atoms cannot be moved outside the fragment that contains it. If you deleted an atom from a fragment (or a group within a fragment) the model itself is changed.

Bonds
Bond objects do not appear by default in the model explorer. To display bonds, go to **File>Preferences**. In the **GUI** tab, select **Show Bonds**.

Fragments
Each structure displayed in the model window is listed as a *fragment* in the model explorer (ions may be listed as multiple fragments). When you expand a fragment list in the model explorer, the atoms the fragment contains are shown. The fragment represents the highest level parent object in a model and typically represent an entire structure. If your model consists of several structures, the model explorer displays a fragment for each one. Fragments represent separate parts of the model; if you start at an atom in one fragment, you cannot trace through a series of bonds that connect to an atom in another fragment. If you create a bond between two such atoms, ChemBio3D will collapse the hierarchical structure to create one fragment. Fragment objects typically consist of chains and groups, but may also contain individual atoms and bonds.

Chains in PDB files
Chains are special groups found in PDB files. In ChemBio3D, chains and groups are functionally identical. If you rename a group as a chain, or vice versa, the icon will change. All group commands also apply to chains.

Solvents
The solvent object group contains all the solvent molecules in the model. The individual molecules appear as child groups within the solvent object. A solvent object should not be a child of any other object.

Note: *When importing PDB models, solvents may show up in chains. ChemBio3D preserves this structure to save the PDB file again.*

Backbone
The backbone object is a display feature that lets you show the carbon-nitrogen backbone structure of a protein. It appears in the model explorer as a separate object with no children. The atoms and bonds that make up the backbone belong to other chains and groups, but are also virtual children of the Backbone object. This lets you select display properties for the backbone that override the display properties of the chains and groups above them in the hierarchy.

Hiding objects

Each object listed in the model explorer has a color-coded icon next to it. The color signifies the visibility status of the object:
Green: The atom is visible.
Red: The fragment (or atom) is hidden (but still present).
Blue: The fragment (or atom) visibility is inherited from its parent group or fragment.
To change hide or display a fragment or atom:

1. In the model explorer, select the fragment or atom.
2. Select **Visibility** from the context menu and choose an option:

- **Inherit Settings**.
- **Show Fragment** (or **Atom**).
- **Hide Fragment** (or **Atom**).

Selecting objects

You can select atoms and bonds using the model explorer in several ways:

- Select a single atom or bond.
- Select multiple atoms; one atom at a time.
- Define a group of atoms and select the group.
- Select atoms or groups based on distance or radius.

To select an atom in the model explorer, click it. To select more than one atom, hold down either the SHIFT or CTRL key at the same time.
To deselect a selected atom or bond, click the atom in the model explorer while pressing the CTRL key.

Selecting by distance

You can select atoms or groups near a selected atom or group of objects. This feature is useful for, among other things, highlighting the binding site of a protein.
To select atoms or groups by distance:

1. Select an atom or fragment using the model explorer.
2. Right-click the selected object. From the context menu point to **Select** and click an option:
   - **Select Atoms within Distance of Selection** selects all atoms within the specified distance from any part of the current selection.
   - **Select Groups within Distance of Selection** selects all groups with one or more atoms within the specified distance from any part of the current selection.
   - **Select Atoms within Radius of Selection Centroid** selects all atoms within the specified distance of the centroid of the current selection.
   - **Select Groups within Radius of Selection Centroid** selects all groups with one or more atoms lying within the specified distance of the centroid of the current selection.

Note: *Atoms or groups already selected are not included. Also, the current selection will be cleared unless multiple selection is used. Hold the SHIFT key down to specify multiple selection.*

Selecting object color

By default, all atoms are assigned a color that is defined in the Elements table. With the model explorer, you can use different selection highlight colors for different fragments or groups. (The colors defined in the Elements table don't change when you do this.)
In the model explorer, you can change the default color of an object to a custom color.

- To select a custom color, right-click the object and choose **Color**>**Select Color**.
- to revert to the default color, right-click the object in the model explorer and go to **Color**>**Apply Atom Color**>**Inherit Atom Color**.
- To select the custom color again, right-click the object and go to **Color**>**Apply Atom Color**>**Apply Atom Color**.

Groups

You can select two or more atoms in your model and group them in a list in the model explorer. After creating the group, you can color all the atoms in the group, hide them, or change their display mode without having to select each atom. You can also use groups to highlight part of a model (such as the active site of a protein) for visual effect.
Objects in group do not have to be connected to each other in your model and can consist of other groups, atoms, and bonds.
To create a group:

1. Do one of the following:

- In the model explorer, hold down the CTRL key and select atoms you want in the group.
- In the model window, hold the SHIFT key and select the atoms you want in the group.

2. In the model explorer, right-click your selection and choose **New Group** from the context menu.
3. (Optional) Rename the group by typing a new name.

Selecting a group
To select a group, click the group in the model explorer.

Expanding a group
To expand or contract a group, click its '+' or '-' icon.

Adding objects to groups
You can add lower level objects to an existing group, or combine groups to form new groups.
To add to a group:

1. In the model explorer, select the objects you want to add, using either SHIFT+click (contiguous) or CTRL+click (non-contiguous).
2. Right-click your selection and choose **New Group** from the context menu.
3. Rename the group, if desired.

Note: *The order of selection is important. The group or chain to which you are adding must be the last object you select.*

Deleting groups
You can delete the group without affecting its objects or the model. You can also delete the group and all the objects within it.

- Select **Delete Group to** remove the grouping while leaving its contents intact.
- Select **Delete Group and Contents to** delete the group from the model.

Coloring groups
Another way to view models is by assigning different colors to groups. Changing a group color in the model explorer overrides the standard color settings in the Elements table and the Substructures table.
To change a group color:

1. Select a group or groups.
2. Right click the selected group(s) and choose **Color**>**Select Color** on the context menu. The Color Dialog box appears.
3. Choose a color and click **OK**.

To revert to the default color:

1. Select the group or groups.
2. Right-click your selection.
3. On the context menu, go to choose **Color**>**Apply Group Color** and select **Inherit Group Color**.

Resetting defaults
To remove changes, use the **Reset Children to Default** command on the context menu.

Group labels

When you create a group, it is listed using a generic name in the model explorer. You can change the name and display it in the model window.

To set group labels:

1. Go to **View>Model Explorer** if the model explorer isn't open already.
2. In the model explorer, right-click one of the groups in the list.
3. In the context menu, select Group Labels and choose the desired option.

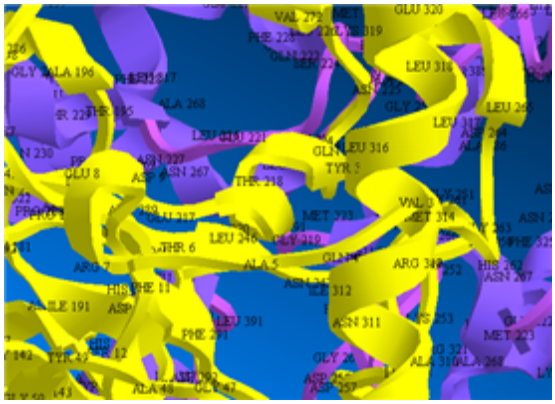


Figure 4.8: group labels

Displaying group labels

You can display group labels in your model. To display labels, right click a group name in the model explorer, click Group Labels in the context menu and select an option:

- Inherit Settings--the label appears if the parent group appears.
- Show Group Label (this group and children)--display the group and child groups.
- Show Group Label (this group only)--display only this group. Does not affect child groups.
- Hide Group label (this group and children)--Hide this group and its child groups.

Moving objects

You group objects together move objects in and out of groups. This becomes useful when you want to highlight different parts of your model or assign attributes. To move an object, click-drag it from one group or another. To move several objects, first select them using either CTRL+click or SHIFT+click.

Nesting objects

You can also put objects in other objects. For example, you can have a DNA fragment that contains two helix groups that, in turn, contains nucleic acid groups.

There are a few things to keep in mind when you move objects:

- You cannot click-drag objects from one fragment to another. (For example, you cannot move atoms from one molecule to another.)
- You cannot rearrange atoms within a group.

Display modes for fragments

Using the model explorer, you can change the display mode for one or more fragments.

1. In the model explorer, select the fragment(s).
2. Right-click in the model explorer window.
3. Go to **Display Mode** and select a display mode option.

For more information, see "Display modes" on page 34.

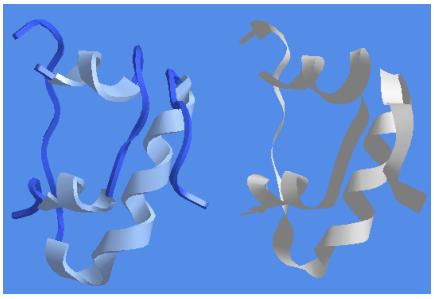


Figure 4.9: Cartoon (left) and ribbon (right) display modes in the model explorer.

Structure browser - adding and removing fragments

You can add or remove fragments from the model explorer into the structure browser. The fragments you add to the structure browser appear in the model window.
To add fragments into structure browser:

1. Go to **View>Model Explorer** if the model explorer isn't open already.
2. In the model explorer, right-click the fragments that you want to add to the structure browser.
3. In the context menu, select **Add to Structure Browser**.

To remove fragments from the structure browser:

1. Go to **View>Model Explorer** if the model explorer isn't open already.
2. In the model explorer, right-click the fragments that you want to remove from the structure browser.
3. In the context menu, select **Remove from Structure Browser**.

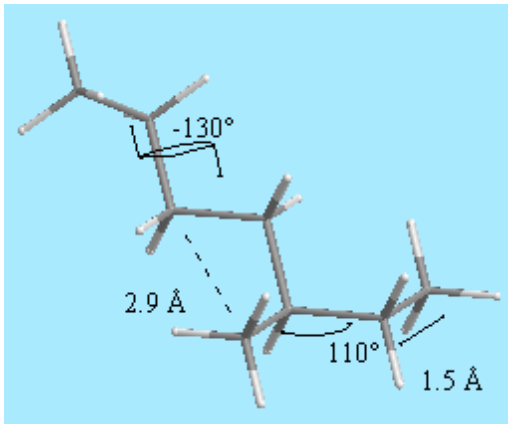
Making fragments exclusive in the structure browser

Model explorer lets you make fragments exclusively available in the structure browser. You can select one or more fragments in the model explorer and make it exclusive in the structure browser. When you make a fragment exclusive in the structure browser, only that item is available in the structure browser.
To make fragments exclusive in the structure browser:

1. Go to **View>Model Explorer** if the model explorer isn't open already.
2. In the model explorer, right-click the fragments that you want to make exclusive in the structure browser.
3. In the context menu, select **Make exclusive in Structure Browser**.

Measuring molecules

You can display atomic distance, bond angles, and dihedral angles in the model window. How to display individual measurements is described in this below. For how to display all measurements in a model, see The measurement table.



To display the distance between atoms:

1. Select the atoms. The atoms do not have to share a bond.
2. Go to **Structure**>**Measurements**>**Display Distance Measurement**.

Tip: *Alternatively, you can select two atoms and hover your cursor over one of the selected atoms. The pop-up window displays the distance.*

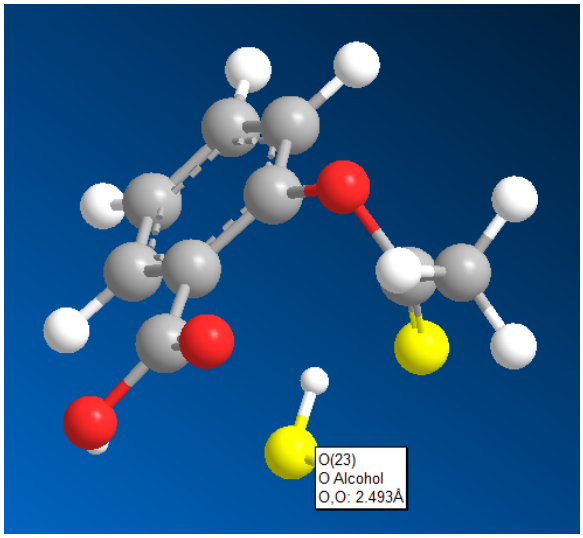


Figure 4.10: The pop-up window displays the distance between atoms in separate fragments.

To display the angle between two bonds:

1. Select either two adjacent bonds or three adjacent atoms.
2. Go to **Structure**>**Measurements**>**Display Bond Angle Measurements**.

To display a dihedral angle:

1. Select either three consecutive bonds or four consecutive atoms that make up a dihedral angle.
2. Go to **Structure**>**Measurements**>**Display Dihedral Measurement**.

By default, measurements in the Model window are displayed to one decimal place. To adjust the measurement values:

1. Go to **File**>**Preferences**.
2. In the **Preferences** dialog box, select the **Measurements** tab.
3. In the **Display decimal places** scroll box, select how many digits past the decimal point you want to appear in the measurement values.
4. Click **OK** when finished.

📝 ***Note:*** *The measurement display value you choose affects values only in the model window.*

The measurement table

The measurement table displays a compiled list of all measurements of your model that you have generated. After you generate the measurements you want, you can select them from the table so that they appear in your model. To open the measurement table, go to **View**>**Measurement Table**.

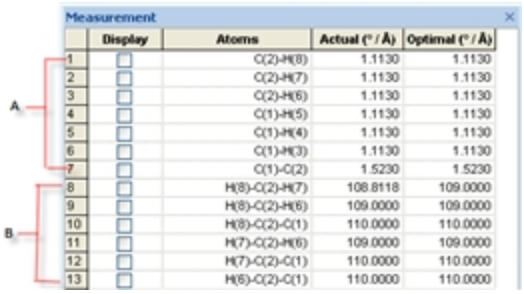


Figure 4.11: The Measurement table: A) Bond lengths; B) Bond angles.

1. To generate measurements, go to **Structure**>**Measurements**>**Generate All** (**Bond Lengths**, **Bond Angles**, **Dihedral Angles**, or **Close Contacts**). The measurement table opens.
2. To enable a measurement to appear in the model window, select its corresponding **Display** check box.

📝 ***Note:*** *You can also modify measurements in the table, see "Setting measurements" on page 77.*

Optimal measurements

Optimal values are used instead of the corresponding standard measurements when a measurement is required in an operation, such as Clean Up Structure. Optimal measurements are used only when the Measurement table is visible. When the Measurement table is not visible, the standard measurements are taken from the parameter tables.
To specify optimal values for measurements, edit the value in the Optimal column.
ChemBio3D also uses the optimal values with the Align command. When you choose **Structure**> **Align**, ChemBio3D reconciles the actual distance between atoms in two fragments to their optimal distances by rigidly moving one fragment relative to the other.

Removing measurements

You can remove information from the Measurement table without affecting the model. Go to **Structure**>**Measurements**>**Clear**.

Displaying atom coordinates

The coordinate tables display the position of each atom in your model. The Internal coordinate table shows the position of each atom relative to the position of another atom. The Cartesian table displays the X-, Y-, and Z-coordinates of each atom relative to a fixed position in space.
To display the Internal coordinates table, go to **View**>**Cartesian Table**.

Internal coordinates (Z -Matrix coordinates)

The first atom in the internal coordinates table is defined as the origin atom. All other atoms in the table are listed with their corresponding positions relative to the origin atom.
To display the internal coordinates table, go to **View**>**Internal Coordinates Table**.
When you select a record in the table, the corresponding atom is selected in the model. Conversely, when you select atoms in the model, the corresponding records are selected in the table.
To change which atom is the origin atom, go to **Structure**>**Set Internal Coordinates**>**Set Origin Atom**.

Cartesian coordinates

The fields in the Cartesian Coordinates table contain the atom name and the X-, Y- and Z- coordinates for each atom. The order of atoms is determined by their serial numbers. All the atoms in a fragment are listed in consecutive records. Hydrogen, lone pair, and dummy atoms are listed last.
As in other tables, you can edit values in the table and the model will update to reflect the change.
To display the Cartesian coordinates table, go to **View**>**Cartesian Table**.

Comparing models by overlay

Use the overlay feature to lay one molecule on top of another. This is useful for when you want to compare structural similarities between models with different compositions or compare conformations of the same model.
For example, assume you want to compare structural similarities between methamphetamine and epinephrine:

1. Go to **File**>**New** to open a new model window.
2. Select the Build from Text tool and click in the model window. A text box appears.

3. Type Epinephrine and press ENTER. A molecule of Epinephrine appears.
4. Click in the model window, below the Epinephrine molecule. A text box appears.
5. Type Methamphetamine and press ENTER. A molecule of methamphetamine appears beneath the epinephrine molecule.

After building the two structures, you must identify at least three pairs of atoms that will be used to apply the overlay. Each pair composes of one atom that you select from each structure.

Note: *Atom Pair consists of two atoms that are a specified distance apart and are in different fragments.*

1. For the first pair of atoms, select the tertiary carbon on the benzene ring in the epinephrine fragment and in the methamphetamine fragment (SHIFT-click both atoms using the Select tool).
2. Go to **Structure**>**Measurements**>**Display Distance Measurement**. The Measurement table appears, showing the distance between the two selected atoms.
3. For the second pair of atoms, in each structure, select the carbon that is opposite the carbon atom you selected for the first pair of atoms.
4. Go to **Structure**>**Measurements**>**Display Distance Measurement**.
5. For the third pair of atoms, select the nitrogen atom in each structure.
6. Go to **Structure**>**Measurements**>**Display Distance Measurement**.

After you define the pairs of atoms, you overlay one structure on the other by setting the distance measurement to zero for each pair of atoms and then perform the overlay calculation.

7. In the Measurement table, type 0 into the **Optimal** column for each atom pair and press ENTER.

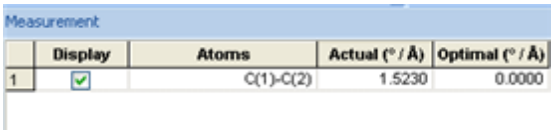


Figure 4.12: Adding optimal values to the Measurement table

8. Go to **Structure**>**Overlay**>**Minimize**. The Overlay dialog box appears.
9. Type 0.100 for the **Minimum RMS Error** and 0.010 for the **Minimum RMS Gradient**.

   The overlay computation will stop when either the RMS Error becomes less than the Minimum RMS Error or the RMS Gradient becomes less than the Minimum RMS Gradient value.
10. Click **Display Every Iteration**.
11. Click **Start**.

How the fragments are moved at each iteration of the overlay computation is displayed.
To stop the overlay computation before it reaches the preset minimum, click **Stop Calculation** on the toolbar. The overlay and recording operation stops.

Molecular surfaces

A molecular surface displays information about an entire molecule, as opposed to the atom and bond information that the structure display provides. Surfaces show a molecule's physical and chemical properties. They display aspects of the external surface interface or electron distribution of a molecule.

Before most molecular surface can be displayed, the data necessary to describe the surface must be calculated using Extended Hückel or one of the methods available in Gaussian.

Solvent accessible surfaces do not require a calculation These surfaces are rendered from data in the parameters tables.

Surface types

The surface types and the calculations necessary to display them are summarized in the table below.

Note: *Spin Density map requires that CS MOPAC or Gaussian computations be performed with an open shell wave function.*

Surface Type	Extended Hückel	CS MOPAC	Gaussian
Solvent Accessible	NA	NA	NA
Connolly Molecular	Yes	Yes	Yes
Total Charge Density	Yes	Yes	Yes
with Molecular Orbital map	Yes	Yes	Yes
with Spin Density map	No	Yes	Yes
with Partial Charges	Yes	Yes	Yes
with Molecular Electrostatic Potential map	No	Yes	Yes
Total Spin Density	No	Yes	Yes
Molecular Electrostatic Potential	No	Yes	Yes
Molecular Orbitals	Yes	Yes	Yes

To display a surface:

1. Perform a suitable calculation using Extended Hückel or Gaussian.
2. Include the **Molecular Surfaces** property calculation whenever it is available.

Note: *Gaussian surfaces calculations are only available for ChemBio3D Ultra.*

Calculation types

Different calculation types can provide different results. If you have performed more than one calculation on a model, for example, both an Extended Hückel and an AM1 calculation, you must choose which calculation to use when generating the surface.

To choose a calculation type:

1. Go to **Surfaces**>**Choose Calculation Result** and select one of your calculations.
2. Go to **Surfaces**>**Choose Surface** and choose a surface types.

   Note: *The Choose Surface commands are toggle switches. Click once to display, click again to turn off the display. You can display more than one surface at a time. When a surface is displayed, its icon is highlighted.*

3. Adjust the display using the surface display tools.

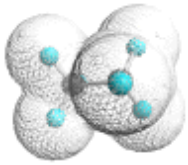
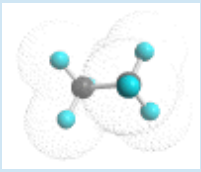
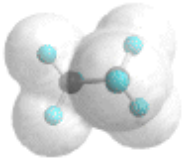
Tip: *If you make a lot of adjustments to the display, activate the Surfaces toolbar and tear off the specific tools you will be using often.*

Not all surfaces can be displayed from all calculations. For example, a Molecular Electrostatic Potential surface may be displayed only following a Gaussian or CS MOPAC calculation. If a surface is unavailable, the command is grayed out in the submenu.

To generate surfaces from CS MOPAC or Gaussian, you must choose Molecular Surfaces as one of the properties calculated by these programs.

Surface display types

ChemBio3D offers four different types of surface displays, each with its own properties. These types are shown in the following table:

Surface Display Type	Description
Solid	The surface is displayed as an opaque form. Solid is a good choice when you are interested in the details of the surface itself, and not particularly interested in the underlying atoms and bonds.
Wire Mesh 	The surface is displayed as a connected net of lines. Wire Mesh is a good choice when you want to focus on surface features, but still want some idea of the atoms and bonds in the structure.
Dots 	The surface is displayed as a series of unconnected dots. Dots are a good choice if you are primarily interested in the underlying structure and just want to get an idea of the surface shape.
Translucent 	The surface is displayed in solid form, but is partially transparent so you can also see the atoms and bonds within it. Translucent is a good compromise between surface display styles.

Surface resolution

The Surface Resolution is a measure of how smooth the surface appears. The higher the resolution, the more points are used to calculate the surface, and the smoother the surface appears. However, high resolution values can also take a long time to calculate. The default setting of 30 is a good compromise between speed and smoothness.
To set the resolution:

1. Go to **Surfaces**>**Resolution**. The **Resolution** slider appears.
2. Adjust the slider to the desired resolution.

The new resolution is the middle value listed at the bottom of the Resolution tool.

Surface colors

Setting the molecular surface color depends on the type of surface.

For setting color in Solvent Accessible, Connolly Molecular, or Total Charge Density surfaces, go to **Surfaces**>**Color Mapping**>**Surface Color** and select the new color.
For Total Spin Density, Molecular Electrostatic Potential, and Molecular Orbital surface types, you must specify two colors. On the **Surfaces** menu, choose **Color A** or **Color B**.

Surface mapping
The Mapping property provides color-coded representations of atom colors, groups of atoms, hydrophobicity, partial charges, and electrostatic potential superimposed on the solvent-accessible surface.
Surface Color. Is the color you have chosen for the molecular surface.
Atom Color. Is based on the displayed atom colors (these may or may not be the default element colors).
Element Color. Is based on the default colors in the Elements Table.
Group Color. Is based on the colors (if any) you specified in the model explorer when creating groups.
Hydrophobicity. Is displayed according to a widely-used color convention derived from amino acid hydrophobicities, where the most hydrophobic (lipophilic) is red and the least hydrophobic (lipophobic) is blue.
Partial Charges and Electrostatic Potential (derived from the partial charges). These properties are taken from the currently selected calculation. If you have performed more than one calculation on the model, you can specify which calculation to use. Go to **Surfaces**>**Choose Result**.

Isovalues
Isovalues are constant values used to generate a surface. For each surface property, values can be calculated throughout space. For example, the electrostatic potential is very high near each atom of a molecule, and vanishes as you move away from it. ChemBio3D generates a surface by connecting all the points in space that have the same value, the isovalue. Weather maps offer other common examples of isovalues in two dimensions, connecting locations of equal temperature (isotherms) or equal pressure (isobars). There are two isovalues to select from, depending on the surface you choose. For the total charge density surface, set the isocharge value; for the molecular orbital surface, se the isocontour value.
Setting an isovalue. To set an isovalue:

1. Go to **Surfaces**>**Choose Surface** and select a surface type.
2. On the Surfaces menu, select either **Iso>contour** or **Iso>charge.**
3. Adjust the slider to the new isovalue.

The new isovalue is the middle value listed at the bottom of the Isocontour tool.

Solvent radius
You can set the solvent radius using the slider. The default solvent radius is 1.4 Å, the value for water. Radii for other common solvents are shown below:

Solvent	Radius (Å)
Water	1.4
Methanol	1.9
Ethanol	2.2
Acetonitrile	2.3
Acetone	2.4
Ether	2.4
Pyridine	2.4
DMSO	2.5
Benzene	2.6
Chloroform	2.7

To set the solvent radius:

1. Go to **Surfaces**>**Solvent Radius**. The **Radius** slider appears.
2. Adjust the slider to the desired resolution.

The new radius is the middle value listed at the bottom of the Radius tool.

Extended Huckel

Extended Hückel is a basic semi-empirical method that you can use to generate molecular surfaces rapidly for most molecular models. Applying an Extended Hückel calculation is a common preliminary step for predicting surfaces using more sophisticated methods.
To compute molecular surfaces using the Extended Hückel method, go to **Calculations**>**Extended Hückel**>**Calculate Surfaces**.

📝 ***Note:*** *Before performing an Extended Hückel calculation, ChemBio3D 13.0 deletes all lone pairs and dummy atoms.*

At this point, a calculation has been performed and the results of the calculation are stored with the model.
To compute partial charges using the Extended Hückel method, go to **Calculations**>**Extended Hückel**>**Calculate Charges**.
For each atom in the model, a message is created listing the atom and its partial charge. If you have selected **Partial Charge** in the **Pop-up Information** tab of the Model Settings dialog box, then the partial charges will appear as part of the pop-up information when you point to an atom.

Solvent-accessible surface

The solvent-accessible surface represents the portion of the molecule that solvent molecules can access.
To determine the solvent-accessible surface, a small probe sphere simulating the solvent molecule is rolled over the surface of the molecule (van der Waals surface). The solvent-accessible surface is defined as the locus described by the center of the probe sphere, as shown in the diagram below.

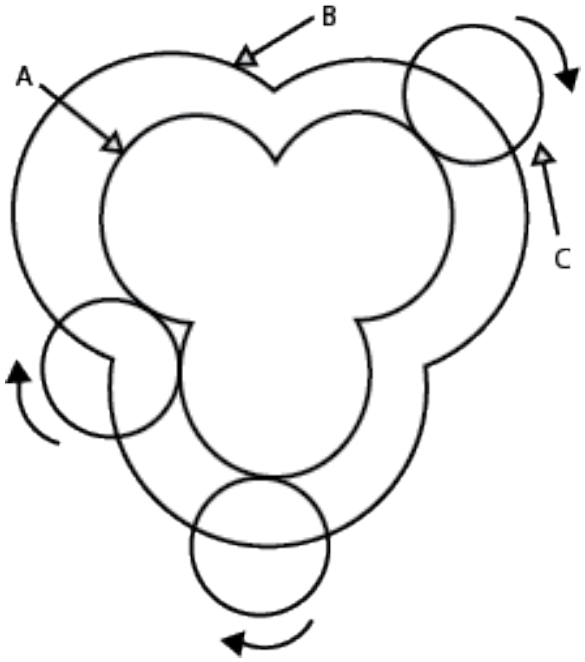


Figure 4.13: van der Waals surfaces: A)van Der Waals surface; B) Solvent Accessible surface; C) Solvent Probe.

Connolly molecular surface

The Connolly surface, also called the molecular surface or solvent-exclude surface is defined as the surface made by the center of a solvent sphere as it contacts the van der Waals surface. The volume enclosed by the Connolly surface is called the solvent-excluded volume.
These surfaces are shown below.

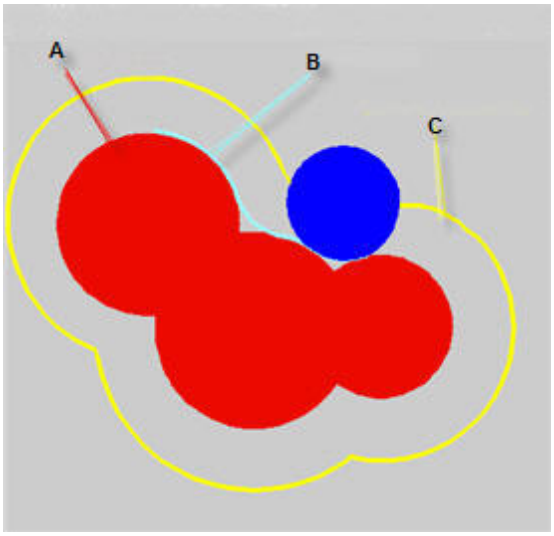


Figure 4.14: Connolly molecular surface: A) van Der Waals surface; B) Connolly surface; C) Solvent accessible.

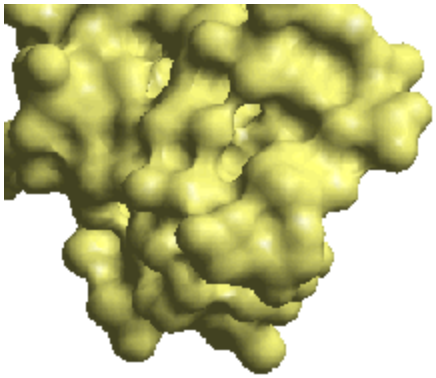


Figure 4.15: Connolly surface of icrn.

Total charge density

The total charge density is the electron density in the space surrounding the nuclei of a molecule, or the probability function for finding electrons in the space around a molecule. The default isocharge value of 0.002 atomic units (a.u.). This value approximates the molecule's van der Waals radius and represents about 95% of the entire three-dimensional space occupied by the molecule.

The total charge density surface is the best visible representation of a molecule's shape, as determined by its electronic distribution. The total charge density surface is calculated from scratch for each molecule and is generally more accurate than the space filling display.

For total charge density surfaces, the properties available for mapping are molecular orbital, spin density, electrostatic potential, and partial charges. The color scale uses red for the highest magnitude and blue for the lowest magnitude of the property. Neutral is white.

You can choose the orbital to map onto the surface with the **Molecular Orbital** tool on the **Surfaces** menu. The orbital number appears in parentheses in the **HOMO/LUMO** submenu.

Molecular orbitals

Molecular Orbital (MO) surfaces visually represent the various stable electron distributions of a molecule. According to frontier orbital theory, the shapes and symmetries of the highest-occupied and lowest-unoccupied molecular orbitals (HOMO and LUMO) are crucial in predicting the reactivity of a species and the stereochemical and regiochemical outcome of a chemical reaction.
Go to **Surfaces**>**Select Molecular Orbital** to see the list of HOMO/LUMO orbitals in the model. Select the orbital you want to view.
You can specify the isocontour value for any computed MO surface using the **Isocontour** tool on the **Surfaces** menu. The default isocontour value for a newly computed surface is the value you last specified for a previously computed surface. If you have not specified an isocontour value, the default value is 0.01.

Total spin density

The total spin density surface describes the difference in densities between spin-up and spin-down electrons in any given region of a molecule's space. The larger the difference in a given region, the more that region approximates an unpaired electron. The relative predominance of spin-up or spin-down electrons in regions of the total spin density surface can be visualized by color when total spin density is mapped onto another surface (total charge density). Entirely spin-up (positive value) electrons are red, entirely spin-down (negative) blue, and paired electrons (neutral) are white. You can use the total spin density surface to examine the unpaired electrons of a molecule. The surface exists only where unpaired electrons are present. Viewing the total spin density surface requires that both spin density and molecular surfaces are calculated by CS MOPAC or Gaussian using an open shell wave function.

Molecular Electrostatic Potential

The Molecular Electrostatic Potential (MEP) represents the attraction or repulsion between a molecule and a proton. Attraction is represented by negative values and repulsion is indicated by positive values. Experimental MEP values can be obtained by X-ray diffraction or electron diffraction techniques, and provide insight into which regions of a molecule are more susceptible to electrophilic or nucleophilic attack. You can visualize the relative MEP values by color when MEP is mapped onto another surface (total charge density). The most positive MEP value is red, the most negative blue, and neutral is white.
For more information on MEP, see "MEP" on page 290.

Partial surfaces

Scientists who study protein-ligand interactions are often interested in generating a molecular surface of a protein that does not include a ligand. ChemBio3D Ultra 13.0 can generate partial Solvent Accessible and Connolly surfaces, either by excluding ligands, or by excluding selected parts of the model, or both.
To generate a partial surface:

1. Go to **Surfaces**>**Advanced Molecular Surfaces**.
2. Select the surface type and what you want to include and exclude in the Advanced Molecular Surfaces dialog box.

Solvent atoms are excluded by default but may be included with the check box. Hidden atoms (usually hydrogens) may also be included or excluded.

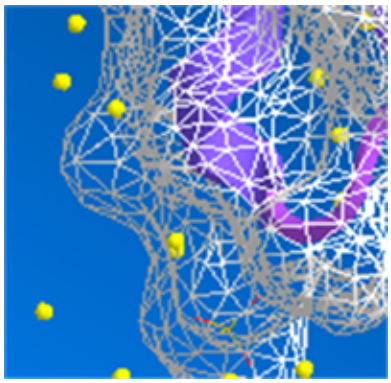


Figure 4.16: Partial surface excluding solvent atoms

After displaying a surface, you can set surface transparency and reflectivity. You can color the surface by atom, element, or group color, or by group hydrophobicity, in addition to monochromatic surfaces of any color.
You can also restrict the surface either by distance from the selected group, or by flooding.

Volume slicing

The volume slicing tool lets you project almost any molecular surface into a 2D Plane. After calculating the surface, you can slice through your model in either the X, Y, or Z planes and adjust the location of the plane as desired.

1. Calculate a desired surface. For more information, see "Molecular surfaces" on page 62.
2. To display the surface go to **Surface**>**Choose Surface** and select the surface to display.

   Note: *The volume slicing tool cannot be applied to Connolly surfaces.*

3. In the Model Display toolbar, select the volume slice button . The volume slicing dialog box appears.
   The volume slicing dialog box includes three sliders that you use to control the locations of each plane in the model window.
4. In the dialog box, select one or more check boxes to display the planes you want to view.
5. Move the sliders to adjust the location for each plane.
6. To orient a plane so that it is facing you (parallel with the screen), click the corresponding button under **Face User**.
   The + button displays one side of the selected plane; the - button displays the opposite side.
7. Select or deselect **Show Surface/Orbital** to display or hide the surface.
8. Click **OK** when finished.

Using stereo pairs

Stereo Pairs is a display enhancement technique based on the optical principles of the stereoscope. By displaying two images with a slight displacement, a 3D effect is created.

Note: *a stereoscope is a device for viewing photographs in three dimensions.*

Stereo views can be either parallel or reverse (direct or cross-eyed). Some people find it easier to look directly, others can cross their eyes and focus on two images, creating an enhanced three dimensional effect. In either case, the effect may be easier to achieve on a printed stereo view of your model than on the screen. Keep the images relatively small, and adjust the distance from your eyes.

Setting stereo pair parameters

To set the stereo pairs parameters:

1. Go to **File**>**Model Settings** and click the **Stereo & Depth** tab. The stereo views control panel appears.
2. Select **Render Stereo Pairs** to display two views of the model next to each other. The right view is the same as the left view, rotated about the Y-axis.
3. Specify the **Eye Separation** (Stereo Offset) with the slider. This controls the amount of Y-axis rotation.
4. Specify the degree of separation using the **Separation** slider. About 5% of the width is a typical separation for stereo viewing.

To select whether the views are cross-eyed or direct, do one of the following:

- Select **Reversed** to rotate the right frame to the left. If your left eye focuses on the right-hand model and your right eye focuses on the left-hand model, the two stereo views can overlap.
- Select **Parallel** to rotate the right view further to the right.

Stereo enhancement

ChemBio3D 13.0 provides stereo graphics rendering for hardware that has stereo OpenGL capabilities. There are a variety of stereo graphics cards, stereo glasses, and 3D monitors available.
To activate stereo enhancements:

1. Go to **File**>**Preferences** and select the OpenGL tab.
2. Select **Use Hardware Stereo when Available**.
3. Click **OK**.

Once the hardware is enabled, stereo enhancement is available in any 3D window.

Note: *You must enable "stereo in OpenGL" in the display adapter properties control, as well as in ChemBio3D preferences, and select the correct mode for the glasses/monitor you are using.*

You can use depth fading and perspective with hardware enhancement, but should not activate other stereo modes.

Controlling separation

You can adjust the stereo effect by adjusting the eye separation.

1. Go to **File**>**Model Explorer** and select the **Stereo & Depth** tab.
2. Under **General Stereo Settings**, adjust the Eye Separation slider.
3. Click **OK**.

Setting view focus

As models become large, keeping track of the section on which you are working becomes more difficult. Using the View Focus feature, you can set the focus on selected atoms so that you can pan to the atoms as desired.
To set the view focus:

1. Select the fragment or set of atoms or bonds.
2. Go to **View**>**View Focus**>**Set Focus to Selection**.

After you set the view focus, if you continue building the model with the bond tools, ChemBio3D will resize and reposition the view so that all the atoms in the view focus are always visible. As new atoms are added to the current model, they become part of the view focus.
When rotating or resizing the view manually, the rotation or resize will be centered around the view focus.
To set the view focus at the center of the Model window, go to **View**>**View Position**>**Center View on Focus**.
To place the selected atoms of your model at the center of the Model window, go to **View**>**View Position**>**Center View on Selection**.

Building Advanced Models

The advanced building features in ChemBio3D include options for enhancing your basic model structure, defining your own building parameters, and building models using data and structures from other sources.

Dummy bonds and dummy atoms

A dummy bond lets you specify a connection between two atoms without a defined bond type. Dummy bonds are often used in coordination complexes for inorganic compounds, where another element might be substituted. Dummy atoms are also useful for positioning atoms in a Z-matrix to export to other applications for further analysis. This is helpful when models become large and connectivities are difficult to specify.

📝 ***Note:*** *Dummy bonds and dummy atoms are ignored in all computations.*

To add a dummy bond and dummy atom:

1. Select the Dummy Bond tool.
2. Point to an atom and drag from the atom. A dummy bond and a dummy atom are added to the model. The atom created is labeled Du, the ChemBio3D element symbol for dummy atoms.

To add only a dummy atom:

1. Select an existing atom.
2. Using the Build from Text tool, click the selected atom. A text box appears.
3. In the text box, type Du and press ENTER.

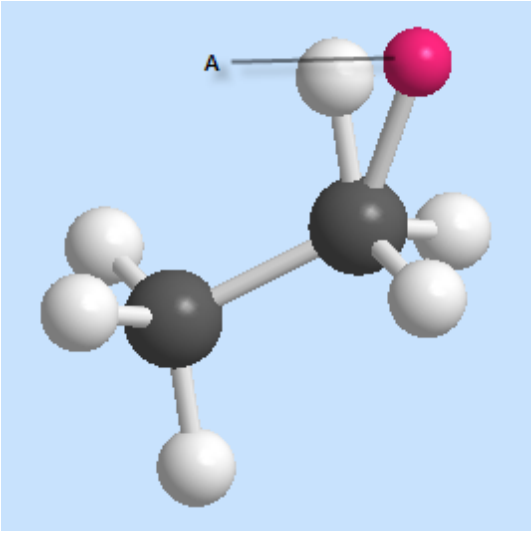


Figure 5.1: A) Dummy atom.

Substructures

For large models, you may consider using *substructures* rather than building models one atom at a time. A substructure is a defined group of atoms such as a ring system, residue, or another structural feature. For example, you can use the Benzyl substructure to add a benzene ring or COOH to add a carboxylic acid functional group. All the substructure definitions are stored in the Substructure parameters table.
For more information, see "Substructures table" on page 143.

Building models from substructures

To copy/paste a substructure to the model window:

1. To open the substructures parameter table, go to **View**>**Parameter Tables**>**Substructures**.
2. In the substructure table, select either the cell or the entire row that contains the substructure name.
3. Right-click the selected cell or row and select **Copy** from the context menu.
4. In the model window, type CTRL+V or right-click the window and select **Paste** from the context menu.

You can also use the text tool:

1. Using the Build from Text tool, click in the model window.
2. In the text box, type the name of the substructure and press ENTER. The substructure appears in the model window.

Note: *The substructure table need not be open to use the text tool.*

Adding a substructure to a model

To attach a substructure to an existing model:

1. In the model, select the atom where you want to attach the substructure.

   Note: *The atom you select will be replaced with the substructure.*

2. Right-click the selected atom and select **Replace with Text Tool**.
3. In the text box, enter the name of the substructure and press ENTER.

Tip: *Go to **View**>**Parameter Tables**>**Substructures** for a list of substructure names.*

Examples for using substructures

Several examples for using substructures appear below.

Example 1. Building ethane
To build a model of ethane using a substructure:

1. Using the Build from Text tool, click in the model window.
2. Type Et or EtH into a text box with no atoms selected.
3. Press ENTER. A model of ethane appears.

Note: *When automatic rectification is on, the free valence in the ethyl group is filled with a hydrogen. If automatic rectification is off, you need to type* EtH *to get the same result. For substructures with more than one atom with an open valence, explicitly specify terminal atoms for each open valence.*

Example 2. Building with a substructure and other elements

To build a model with substructures and other elements:

1. Using the Build from Text tool, click in the model window.
2. Type PrNH2 into a text box with no atoms selected.
3. Press ENTER. A model of propylamine appears.

Example 3. Polypeptides

To use substructures for building biopolymers, such as proteins:

1. Type HAlaGlyPheOH into a text box with no atoms selected. The additional H and OH cap the ends of the polypeptide. If you don't cap the ends and automatic rectification is on, ChemBio3D tries to fill the open valence.

   Note: *For amino acids that repeat, avoid re-typing the amino acid by putting parenthesis around the repeating unit followed by the number of times it repeats. For example, type HAla(Pro)10GlyOH.*

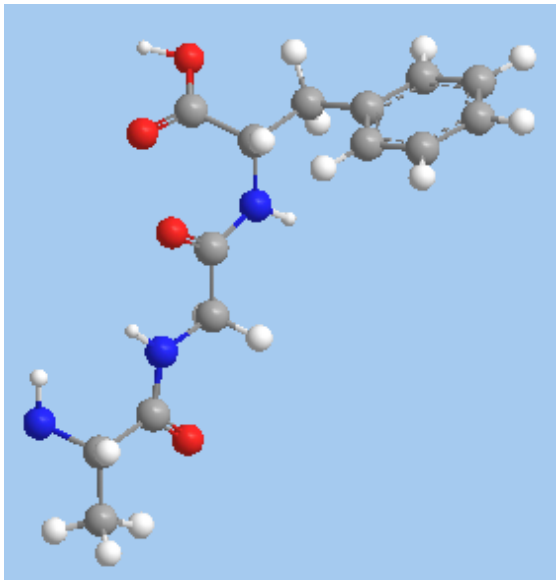
2. Press ENTER.

   Note: *If the substructure contains two or more open valences, ChemBio3D 13.0 creates a bond between the open valence sites to create a ring.*

The alpha form of the neutral polypeptide chain composed of Alanine, Glycine, and Phenylalanine appears.

Note: *You can use the amino acid names preceded with a ß– to obtain the beta conformation, for example* Hß–Alaß–Glyß–PheOH. *To generate the ß character, type ALT+0223 using the number pad.*

The appropriate bonding and dihedral angles for each amino acid are preconfigured in the substructure.



HAlaGlyPheOH polypeptide model.

Tip: *To view the alpha helix formation better, use the Rotate Tool to reorient the model to an end-on view.*

To change the polypeptide to a zwitterion:

1. Select the Build from Text tool.
2. Click the terminal nitrogen. A text box appears over the nitrogen atom.
3. Type + and press ENTER.

The charge is applied to the nitrogen atom. Its atom type changes and a hydrogen atom is added.

4. Click the terminal oxygen.

A text box appears over the oxygen atom.

5. Type - in the text box and press ENTER.

The charge is applied to the oxygen atom. Its atom type changes and a hydrogen atom is removed.

Example 4. Other Polymers

To build the model of a Polythylene Terephthalate (PET) with four units, type OH(PET)4H into a text box with no atoms selected and press ENTER. The H and OH are added to cap the ends of the polymer. The PET model is shown below:

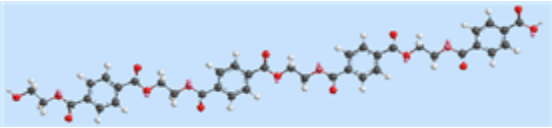


Figure 5.2: A PET polymer with four units.

Bonding by proximity

Atoms within a specified distance (the bond proximate distance) from one another can be automatically bonded. ChemBio3D determines whether two atoms are proximate based on their Cartesian coordinates and the standard bond length measurement.

Pairs of atoms whose distance from each other is less than the standard bond length, plus a certain percentage, are considered proximate. The lower the percentage value, the closer the atoms have to be to the standard bond length to be considered proximate. Standard bond lengths are stored in the Bond Stretching Parameters table.

To set the percentage value:

1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. Select the **Model Building** tab.
3. Use the Bond Proximate Addition% slider to adjust the percentage added to the standard bond length when ChemBio3D assesses the proximity of atom pairs.

You can adjust the value from 0 to 100%. For example, if the value is 50, then two atoms are considered proximate if the distance between them is no greater than 50% more than the standard length of a bond connecting them. If the value is zero, then two atoms are considered proximate only if the distance between them is no greater than the standard bond length of a bond connecting them.
To create bonds between proximate atoms:

1. Select the atoms between which you want to create a bond.
2. Go to **Structure**>**Bond Proximate**.

If the two selected atoms are proximate, a bond is created.

Setting measurements

When you build a model, ChemBio3D uses a set of standard length and angle measurements to determine where to locate atoms in relation to each other. You can override the standard measurements as desired.
To view the standard measurements used in your model, go to **Structure**>**Measurements**>**Generate All** (**Bond Lengths** or **Bond Angles**). Standard measurements appear in the optimal (or equilibrium) column in the Measurement table. To edit a measurement values in your model, replace the desired value in the Actual column of the measurement table and press ENTER.
You are not limited to viewing only the standard measurements. You can also display distances between dihedral angles and non-bonded atoms. For how to modify measurements, see "Setting constraints" on page 79.

Setting bond lengths

You can set the lengths between two atoms that share a covalent, ionic, or hydrogen bond.

To set the length of a bond between two atoms:

1. Select the two atoms.
2. Go to **Structure**>**Measurements**>**Display Distance Measurement**. The Measurement table appears, displaying the distance between the atoms.
3. Click and edit the value in the **Actual** column.
4. Press ENTER.

Setting bond angles

To set a bond angle:

1. Select the three contiguous atoms that define the angle.
2. Go to **Structure**>**Measurements**>**Display Bond Angle Measurement**. The Measurement table appears, displaying the angle value.
3. Click and edit the value in the **Actual** column.
4. Press ENTER.

Setting dihedral angles

To set a dihedral angle:

1. Select four contiguous atoms that define the dihedral angle.

   Note: *The first atom you select will move when the bond rotates.*

2. Go to **Structure**>**Measurements**>**Display Dihedral Measurement**. The Measurement table appears, displaying the angle value.
3. Click and edit the value in the **Actual** column.
4. Press ENTER.

Setting close contact distances

Atoms that do not share a bond are considered close contacts.
To set the distance between two close contact atoms:

1. Select any two atoms that do not share a bond.

   Note: *The atom you select last moves when you set the distance between the atoms you select.*

2. Go to **Structure**>**Measurements**>**Display Distance Measurement**. The Measurement table appears, displaying the distance between the two atoms.
3. Click and edit the value in the **Actual** column.
4. Press ENTER.

Note: *You can also move atoms using the Move Objects tool. The Measurement table will automatically updated to reflect their new positions.*

Atom movement

When you change the value of a measurement, the last atom you selected moves. ChemBio3D repositions the atoms that are attached to the moving atom and excludes atoms that are attached to other selected atoms.
If all the atoms in a measurement are in a ring, the set of moving atoms is generated as follows:

- Only one selected atom that describes the measurement moves.
- If you set a bond length or distance between two atoms, all atoms bonded to the non-moving selected atom do not move. Any atoms bonded to the moving atom move.
- If the Rectify check box in the Model Building tab (go to **File**>**Model Settings** and select the **Model Building** tab) is selected, rectification atoms that are positioned relative to an atom that moves may also be repositioned.

For example, consider this structure:

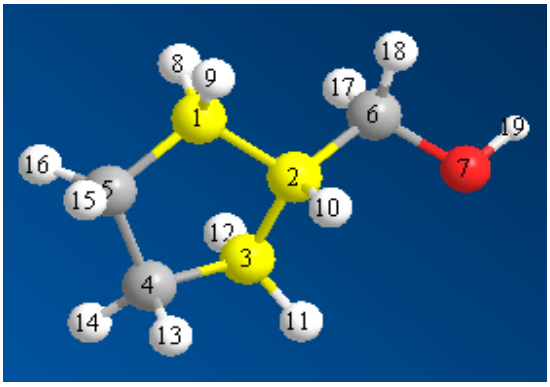


Figure 5.3: Cyclopentylmethanol model.

If you set the bond angle C(1)-C(2)-C(3) to 108 degrees, C(3) becomes the moving atom. C(1) and C(2) remain stationary. H(11) and H(12) move because they are bonded to the moving atom. If the Automatically Rectify check box is selected, H(10) may move because it is a rectification atom and is positioned relative to C(3).

Setting constraints

You can override the standard measurements that ChemBio3D uses to position atoms by setting constraints. You can use constraints for a particular bond length, bond angle, dihedral angle, or non-bonded distance. The constraint is then applied instead of the standard measurement when you use **Clean Up** or perform an aligning, overlay, or MM2 computation.

To set constraints, enter a new value in the **Optimal** field of the Measurement table.

For dihedral angles and non-bonded distances, constraints keep that measurement constant (or nearly so) while the rest of the model is changed by the computation. The constraint doesn't remove the atoms from a computation.

Atom and building types

Building types define the structure of your model– the bond lengths, bond angles, and relative sizes of the atoms themselves. By default, ChemBio3D assigns building types as you build your model using a predefined set of building types. However, you can also create your own building types.

Where Building types define the structural aspects of a model, atom types define attributes such as bond energies, thermal properties, and other nonstructural properties. Force fields use the data to calculate properties of your model and predict model behavior.

Force field calculations take into account the type of each atom in your model, the atom location, and the functional group to which the atom belongs. For example, a carboxyl carbon has a different atom type than an alkyl carbon. For more information on how to add atom types to ChemBio3D, see "Modifying parameter tables" on page 139.

About Correct Atom Types. Correct atom types determine whether atom types are assigned to each atom as you build. Atom types, such as C Alkane specify the valence, bond lengths, bond angles, and geometry for the atom.

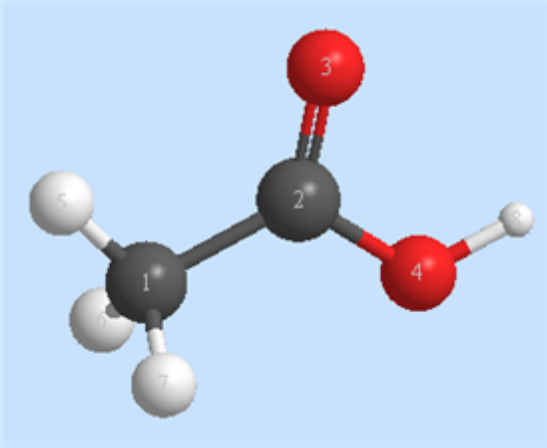
Building type characteristics

The characteristics of an atom must match these type characteristics for ChemBio3D to assign the building type to the atom.

- The atomic symbol.
- The bound-to type (if specified for the building type).
- The bound-to order (if the bound-to type is specified).
- The number of double, triple and delocalized bonds.

Note: *For comparing bond orders, a building type that contains one double bond may be assigned to an atom that contains two delocalized bonds, such as in benzene.*

If the maximum ring size field of a building type is specified, then the atom must be in a ring of that size or smaller to be assigned the corresponding building type.
If an atom is bound to fewer ligands than are specified by a building type geometry but the rectification type is specified, then the atom can be assigned to that building type. Open valences are filled with rectification atoms.
For example, consider the building types for the structure of ethanoic acid:



O(3) matches the criteria specified for the building type O Carbonyl. Specifically, it is labeled 'O', it is bound to a C carbonyl by a double bond; and, it is attached to exactly one double bond and no triple bonds.
If an atom can be assigned to more than one building type, building types are assigned in this order:

1. Building types whose bound-to types are specified and are not the same as their rectification types.
2. Building types whose bound-to types are specified and are the same as their rectification types.
3. Building types whose bound-to types are not specified.

For example, in the model depicted above, O(4) could be one of several building types. First, it could be an O Ether atom for which the bound-to type is unspecified (priority number 3, above). Alternatively, it could be an O Alcohol for which the bound-to type is the same as the rectification type, H Alcohol (priority number 2, above). A third possibility is O Carboxyl, for which the bound-to type is C Carbonyl and the rectification type is H Carboxyl (priority number 1).

Because the characteristic of a specified bound-to type that is not the same as the rectification type (number 1 in the priority list above) is given precedence over the other two possibilities, the O Carboxyl building type is assigned to the oxygen atom.

Changing building types

You can use a text box to change the building type and bonding characteristics. For example, you can change an alkane to an alkene.
To change the building type of some atoms:

1. Click a carbon atom using the Build from Text tool. A text box appears.
2. SHIFT+click an adjacent carbon atom. Both atoms are selected.
3. Click inside the text box and type C Alkene.
4. Press ENTER.

The building type and the bond order are changed to reflect the new model. You can point at the atoms and bonds to display this new information.

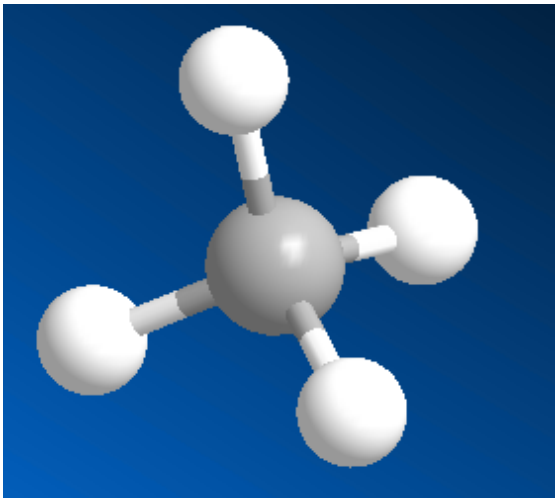
Assigning building types

The easiest way to build models is to allow ChemBio3D 13.0 to assign building types to atoms as you build.
To allow building types to be assigned as you build:

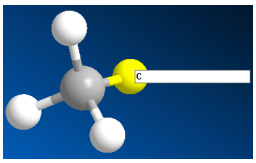
1. Go to **File**>**Model Settings**. The Model Settings dialog box appears.
2. In the **Model Settings** dialog box, select the **Model Building** tab.
3. Select the **Correct Building Type** check box.
4. Click **OK**.

If the **Correct Building Type** check box is selected, building types are corrected when you add, delete, or replace atoms or bonds.
Example:

1. Build a methane model, as shown:

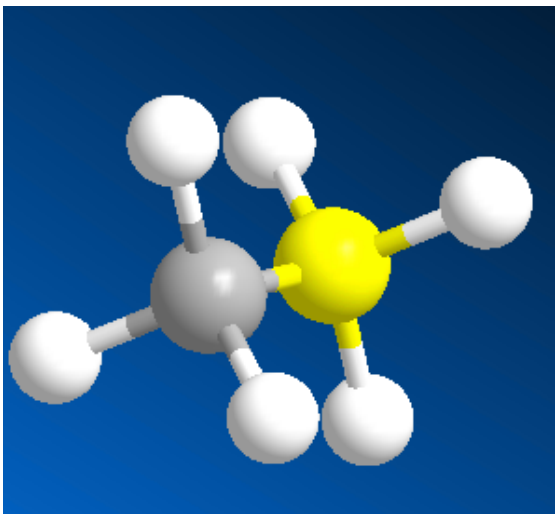


2. Click the **Build from Text** tool.
3. Click a hydrogen atom. A text box appears as shown below:

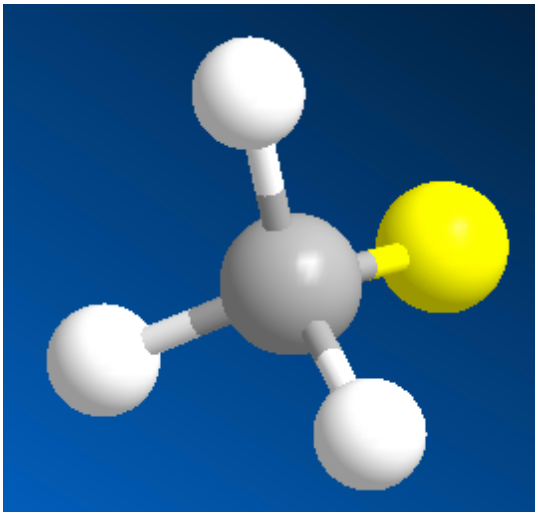


4. Type **C** in the text box and press ENTER.

   If the **Correct Building Type** check box is selected, this figure appears:



   If the **Correct Building Type** check box is not selected, this figure appears:



As depicted in the above example, when building types are assigned and you replace atoms, ChemBio3D attempts to assign the best type to each atom by comparing the information about the atom (such as its symbol and the number of bonds) to each record in the Atom Type table.
In addition, the building types of pre-existing atoms may change when you replace atoms of one type with other atoms of a different type.

Defining building types

In a few instances, you may want to define your own building types, whether to add to the building types table for building or to add to a file format interpreter for importing.
To define your own building types:

1. Go to **View**>**Parameter Tables**>**Chem3D Building Atom Types.** The Chem3D Building Atom Types table opens in a window.
2. To edit a building type, click in the cell that you want to change and type new information.
3. Enter the appropriate data in each field of the table. Be sure that the name for the parameter is not duplicated elsewhere in the table.
4. Close and save the table. You now can use the newly defined building type.

Stereochemistry

You can alter the stereochemistry of your model by inversion or reflection.

Inversion

Inversion repositions side chains extending from a chiral atom that you select.
For example, assume you want to invert N-methylcyclohexylamine around the C(2) carbon (highlighted below):

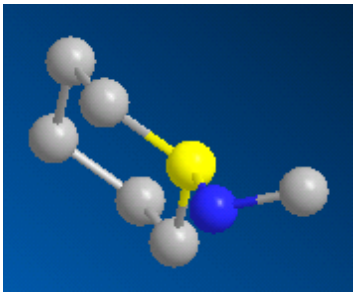


Figure 5.4: N-Methylcyclohexylamine with the C(2) atom selected.

The inverted structure becomes:

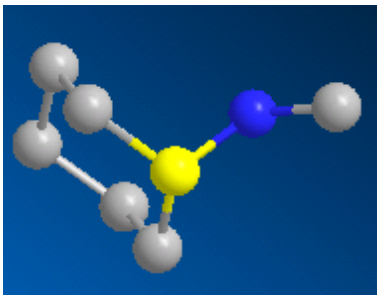


Figure 5.5: Inverted N-Methylcyclohexylamine model

To invert symmetry around a chiral atom:

1. Select the atom.
2. Go to **Structure**>**Invert**.

To invert several dihedral angles (such as all of the dihedral angles in a ring) simultaneously:

1. Select the dihedral angles to invert.
2. Go to **Structure**>**Invert**.

All of the dihedral angles that make up the ring are negated. Atoms positioned axial to the ring are repositioned equatorial. Atoms positioned equatorial to the ring are repositioned axial.

Reflecting a model

Use the Reflect command to reflect through either the X-Y, X-Z, or Y-Z plane or through the model origin (The planes and origin are defined by the view axes not the model axes).
To reflect a model:
Go to **Structure**>**Reflect Model** and select an option:

- **Through X-Y Plane**
- **Through X-Z Plane**
- **Through Y-Z Plane**

- **Invert through Origin**

When you reflect your model through a plane, the coordinates of the third axis are negated. You can choose **Invert through Origin** to negate all of the Cartesian coordinates of the model.
If the model contains a chiral center, reflection changes the model into its enantiomer. In addition, all the Pro-R positioned atoms become Pro-S and all the Pro-S positioned atoms become Pro-R. All dihedral angles used to position atoms are negated.

Note: *Pro-R and Pro-S in ChemBio3D are not equivalent to the specifications R and S used in standard chemistry terminology.*

For example, for the structure shown below, when any atom is selected, go to **Structure>Reflect Model Through X-Z Plane**.

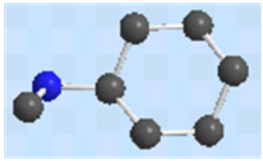


Figure 5.6: Reflecting through a plane

ChemBio3D produces this enantiomer:

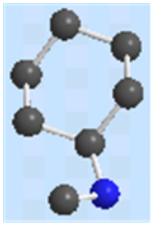


Figure 5.7: Enantiomer produced by reflection

Building with Cartesian tables

The Cartesian table displays the coordinates of each atom in your model relative to the model axes origin. One way to build a new model is to paste Cartesian coordinates from a spreadsheet (or some other table) into an empty ChemBio3D Cartesian table. After you paste the data, ChemBio3D applies minimization parameters and atom types to determine the structure of the model.
To copy Cartesian (Z-matrix) coordinates into ChemBio3D:

1. Select the table in the text or spreadsheet file.
2. Press CTRL+C to transfer data to the clipboard.
3. Go to **View**>**Cartesian Table**. The table opens.
4. Right-click in a blank Cartesian table and select **Paste**.

Example 1: chloroethane Cartesian table

(space character as separator)

```
C 0 -0.464725 0.336544 0.003670
C 0 0.458798 -0.874491 0.003670
Cl 0 0.504272 1.818951 0.003670
H 0 -1.116930 0.311844 0.927304
H 0 -1.122113 0.311648 -0.927304
H 0 -0.146866 -1.818951 0.003670
H 0 1.116883 -0.859095 0.923326
H 0 1.122113 -0.858973 -0.923295
```

Example 2: ethane Cartesian table (tab as separator)

```
C -0.4956 0.5782 0.0037
C 0.4956 -0.5782 0.0037
H 0.0552 1.5557 0.0037
H -1.1517 0.5252 0.9233
H -1.1569 0.5248 -0.9233
H -0.0552 -1.5557 0.0037
H 1.1517 -0.5252 0.9233
H 1.1569 -0.5248 -0.9233
```

Example 3: ethenol Z-Matrix table (tab as separator)

```
C
C 1 1.33
O 2 1.32 1 119.73
H 3 0.978 2 109 1 180
H 2 0.99 1 119 3 180
H 1 0.989 2 119.5 3 180
H 1 0.988 2 119 3 0
```

Building models using ISIS/Draw

To build a model using ISIS/Draw:

1. Draw a structure in ISIS/Draw.
2. Copy the structure to the clipboard.
3. In ChemBio3D, go to **Edit**>**Paste.**

Note: *You can paste a model from ISIS/Draw into the Model Window, but not into the ChemDraw panel. After your model appears in the Model Window, you can synchronize the window so that the drawing appears in the ChemDraw panel.*

Lone electron pairs

Some molecules, such as amines and carboxylic acids, have lone electron pairs that you can add or remove when modifying your model. After you add an electron pair, you can show or hide the electrons without chemically changing your model.

Adding lone pairs

To add a lone electron pair to your model, go to **Structure**>**Lone Pairs**>**Add.**

Removing lone pairs

To remove an electron pair, go to **Structure**>**Lone Pair** and select **Remove.**

Showing/hiding lone pairs

You can specify whether electron pairs are hidden or displayed.

Note: *Hidden electron pairs are still part of the model.*

To show or hide lone pairs, do one of the following:

- Go to **Structure**>**Lone Pair** and select either **Add, Show** or **Hide.**
- Go to **View**>**Model Display**>**Show Lone Pairs** and select either **Hide** or **Show**.

Computational Engines

Computational chemistry applies chemistry, mathematics, and software to solve chemical problems. It includes methods for calculating molecular properties or simulated experimental results.
Computational methods can be classified into these categories:

- Force field calculation methods
- Ab initio methods
- Semi-empirical methods

The applications that implement these methods are called computational engines. This section discusses several computational engines: MM2, MMFF94, Gaussian, CS MOPAC, and CS GAMESS.
None of these methods is best for all purposes nor do any of them implement all three computational categories. You must choose a method and a computational engine that suits your needs.
The choice of method depends on several factors including:

- The nature and size of the molecule.
- The type of information sought.
- The availability of applicable experimentally determined parameters (as required by some methods).
- Computer resources.

To determine which engine to use to calculate a particular property, see Chemical Properties.

Ab initio methods

Ab initio methods are computational methods based on quantum chemistry. In these methods, molecular structures can be calculated using the Schrödinger equation, values of the fundamental constants, and atomic numbers of the atoms present.
The computational engines Gaussian and CS GAMESS apply *ab initio* methods.

Semi-empirical methods

Semi-empirical methods use approximations from experimental data to provide the input into the mathematical models.
The CS MOPAC and Gaussian computational engines use semi-empirical methods.

Force field calculation methods

A force field refers to the form and parameters of the calculations used to predict molecular properties. For example, you can use a force field calculation to predict the torsional constraint for a bond or the repulsion between molecules. Force fields are used for a variety of calculations and are often verified with experimental values.

Compute properties

Calculation of the energy of a molecule at a specific geometry is called single point energy computation. Compute Properties represents a single point energy computation that reports the total steric energy for the current conformation of a model.

Note: *The Steric Energy is computed at the end of an MM2 Energy minimization.*

A comparison of the steric energy of various conformations of a molecule gives you information on the relative stability of those conformations.

Note: *If parameters are not available because the atom types in your model are not among the MM2 atom types supported, ChemBio3D will approximate. You can view the approximate parameters using the Show Used Parameters command after the analysis is complete.*

Compare the steric energies of *cis*- and *trans*-2-butene.
To build *trans*-2-butene and compute properties:

1. Go to **File**>**New.**
2. Select the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type trans-2-butene and press ENTER.

A molecule of *trans*-2-butene appears in the model window.

5. Go to **Calculations**>**MM2**>**Compute Properties**. The Compute Properties dialog box appears.
6. Click **Run**.

When the steric energy calculation is complete, the individual steric energy terms and the total steric energy appear in the Output window. Use the Output window scroll bar to view all of the output. The units are kcal/mol for all terms. At the beginning of the computation the first message indicates that the parameters are of Quality=4, which means that the results are experimentally determined and verified.

Note: *The energy values are approximate and can vary slightly based on the type of processor used to calculate them.*

These values appear:

- *Stretch* represents the energy associated with distorting bonds from their optimal length.
- *Bend* represents the energy associated with deforming bond angles from their optimal values.
- *Stretch-Bend* term represents the energy required to stretch the two bonds involved in a bond angle when that bond angle is severely compressed.
- *Torsion* term represents the energy associated with deforming torsional angles in the molecule from their ideal values.
- *Non-1,4 van der Waals* term represents the energy for the through-space interaction between pairs of atoms that are separated by more than three atoms.

For example, in *trans*-2-butene, the Non-1,4 van der Waals energy term includes the energy for the interaction of a hydrogen atom bonded to C(1) with a hydrogen atom bonded to C(4).

- *1,4 van der Waals* represents the energy for the through-space interaction of atoms separated by two atoms. For example, in *trans*-2-butene, the 1,4 van der Waals energy term includes the energy for the interaction of a hydrogen atom bonded to C(1) with a hydrogen atom bonded to C(2).
- The Dipole/Dipole steric energy represents the energy associated with the interaction of bond dipoles. For example, in *trans*-2-butene, the Dipole/Dipole term includes the energy for the interaction of the two C Alkane/C Alkene bond dipoles.

We can use a force field method to compare steric energy values in *cis*-2-butene to those in the *trans* isomer.
To build a *cis*-2-butene and compute properties:

1. Go to **Edit**>**Clear** to delete the model.
2. Double-click in the model window. A text box appears.
3. Type `cis-2-butene` and press ENTER.

   A molecule of *cis*-2-butene appears in the model window.
4. Go to **Calculations**>**MM2**>**Compute Properties**. The steric energy terms for *cis*-2-butene appears in the Output window.
5. Click **Run**.

Repeat steps 1-5 to build the trans isomer (enter `trans-2-butene` in step 3.)
Below is a comparison of the steric energy components for *cis*-2-butene and *trans*-2-butene.

Energy Term	**trans-2-butene** (kcal/mol)	**cis-2-butene** (kcal/mol)
stretch	0.0627	0.0839
bend	0.2638	1.3235
stretch-bend	0.0163	0.0435
torsion	-1.4369	-1.5366
non-1,4 van der Waals	-0.0193	0.3794
1,4 van der Waals	1.1742	1.1621
dipole/dipole	0.0767	0.1032
total	0.137	1.5512

The significant differences between the steric energy terms for *cis* and *trans*-2-butene are in the bend and Non-1,4 van der Waals steric energy terms. The bend term is much higher in *cis*-2-butene because the C(1)-C(2)-C(3) and the C(2)-C(3)-C(4) bond angles must be deformed from their optimal value of 122.0° to 127.4° to relieve some of the steric crowding from the interaction of hydrogens on C(1) and C(4). The interaction of hydrogens on C(1) and C(4) of *trans*-2-butene is much less intense, thus the C(1)-C(2)-C(3) and the C(2)-C(3)-C(4) bond angles have values of 123.9°, much closer to the optimal value of 122.0°. The Bend and Non-1,4 van der Waals terms for *trans*-2-butene are smaller, therefore *trans*-2-butene has a lower steric energy than *cis*-2-butene.

Calculating multiple properties

The Property Picker lets you compute multiple chemical, topological, and thermodynamic properties using multiple calculation engines. For information on specific properties that you can calculate, see "Chemical properties" on page 216.

To apply the property picker:

1. Go to **Calculations**>**Compute Properties**. The Property Picker dialog box appears. In this dialog box, the properties are classified into categories, such as GAMESS Interface and Molecular Topology.
2. Expand the desired category/categories and select the check boxes corresponding to the properties that you want to calculate.
3. Click **OK**. The selected properties appear in the Output window.

MM2 and MMFF94

MM2 and MMFF94 apply force field calculation methods. These engines are designed to calculate steric energy, thermal energy, and other values. Results are saved as part of the atom properties.

MM2 and MMFF94 may be viewed as different calculation techniques you use to return a result. Which technique you use depends on your type of model and the properties you want to calculate.

MM2

MM2 is most commonly recommended for calculating properties of small organic models. The MM2 procedures assume that you understand how the potential energy surface relates to conformations of your model. If you are not familiar with these concepts, see "MM2 references" on page 291.

MM2 parameters

The MM2 parameters are listed in the MM2Atom Types table. To view the table, go to **View**>**Parameter Tables**>**MM2 Atom Types**. The original MM2 parameters include elements commonly used in organic compounds: carbon, hydrogen, nitrogen, oxygen, sulfur, and the halogens. The atom type numbers for these atom types range from 1 to 50.

The rest of the parameters consist of atom types and elements in the periodic table that were not included in the original MM2 force field (such as metals).

The atom type numbers for these atom types range from 111 to 851. The atom type number for each of the non-MM2 atom types in the MM2 Atom Type Parameters table is based on the atomic number of the element and the number of

ligands in the geometry for that atom type. To determine an atom type number, the atomic number is multiplied by ten, and the number of ligands is added. For example, Co Octahedral has an atomic number of 27 and six ligands. Therefore the atom type number is 276.
In cases where different atom types of the same element have the same number of ligands, the number nine is used for the second geometry (Iridium Tetrahedral, Atom Type # 774 and Iridium Square Planar, Atom Type # 779).
The rectification type of all the non-MM2 atom types in the ChemBio3D Parameter tables is hydrogen (H). For more information on rectification types, see "Building types " on page 140.

Viewing MM2 parameters
To view the parameters that ChemBio3D 13.0 uses to perform MM2 computations, go to **View**>**Parameter Tables**>**MM2 Atom Type Parameters**.

Editing MM2 parameters
You can edit the parameters that come with ChemBio3D. Parameters that you add or change can be guesses, approximations, or values from literature.
In addition, there are several adjustable parameters available in the MM2 Constants table.

Note: *Before editing we recommend that you back up the parameter files in the C3DTable directory.*

For example, to add a new parameter to the Torsional parameters table:

1. Go to **View**>**Parameter Tables**>**Torsional Parameters**.
2. Enter the appropriate data in each field of the parameter table. Be sure that the name for the parameter is not duplicated elsewhere in the table.
3. Close and save the table.

Showing used parameters
You can display in the Output window all parameters used in an MM2 calculation. To show the used parameters, go to **Calculations**>**MM2**>**Show Used Parameters**. The list includes a quality assessment of each parameter. The empirically-derived (highest quality) parameters are rated as 4 while the "best guess" (lowest quality) parameters are rated 1.

Repeating a computation

1. Go to **Calculations**>**MM2**>**Repeat MM2 Job**.
2. Change parameters if desired and click **Run**. The computation proceeds.

MMFF94

Use MMFF94 to perform energy minimization calculations on proteins and other biological structures.

Multiple processors
Molecular modeling force field calculations can become time consuming and impractical for large molecules. You can overcome this problem by using multiprocessors.
To verify that multiple processors are being used:
Go to **Calculations**>**MMFF94**>**Perform MMFF94 minimization**.

In the Preferences tab, select **Enable Multiprocessor support.**

Displaying MMFF94 atom types

You can display the MMFF94 atom types for your model without performing calculations. The Atom Property table lists each atom, its atom type, and its charge.

To view the list of MMFF94 atom types in your model:

1. Go to **View**>**Atom Property Table**.
2. Go to **Calculations**>**MMFF94**>**Set Up MMFF94 Atom Types and Charges**.

Calculating potential energy

You can calculate the potential energy of your model using MMFF94 without performing an energy minimization beforehand.

1. Go to **Calculations**>**MMFF94**>**Calculate MMFF94 Energy and Gradient**.

1. In the dialog box, click **Run**.
2. Go to **View**>**Atom Property Table** to view the results.

The non-bonded energy represents the pair-wise sum of all the energies of all possible interacting non-bonded atoms. It is the sum of van der Waals interactions and coulombic electrostatic interactions among the atoms.

Electrostatic calculations

The electrostatic energy is a function of the charge on the non-bonded atoms of a molecule, their interatomic distance, and a molecular dielectric expression that accounts for the attenuation of electrostatic interaction by the environment. It deals with interactions between particles or atoms that are spatially close and interactions between atoms that are spatially distant from one another. Three methods ares supported (Exact Method, Fast Multipole Method [FMM], Adaptive Tree Code [ATC]) that approximate the electrostatic interactions and hence any cut off method is not required in the calculation.

To perform an electrostatic calculation:

1. Go to **Calculations**>**MMFF94**>**Perform MMFF94 minimization**. The Perform MMFF94 Minimization dialog box appears.
2. Click the **Electrostatic Calculations** tab.
3. Select a calculation method:
   - Set the value of the dielectric constant and the dielectric exponent for exact calculations. The value of dielectric exponent can be 1 or 2.
   - Set the value of Refinement and Expansion level for Fast Multiple Method calculations.
   - Set the value of Order of Taylor expansion, BMAX MAC Acceptance parameter, and Maximum number of particles per node for Adaptive Tree Code calculations.
4. Click **Run**. The output window displays the calculation result.

Note: *When using either the FMM or ATC, it is strongly recommended that you use one of the Van der Waals cut-off techniques, or the Van der Waals terms will still scale as N2 time where N is the number of atoms.*

van der Waals calculations

van der Waal calculation is a non-bonded energy calculation. Attraction occurs at short range, and rapidly decrease as the interacting atoms move apart even by a few angstroms. Repulsion occur when the distance between interacting atoms becomes even slightly less than the sum of their contact radii. As the number of atoms increases, van der waals calculations may become time consuming. ChemBio3D 13.0 introduces three cut off techniques that prevent van der Waals calculations from scaling in time as the number of atoms increases:

- Shift function
- Switching function
- Truncation function

To perform van der waals calculation:

1. Go to **Calculations**>**MMFF94**>**Perform MMFF94 minimization**. The Perform MMFF94 Minimization dialog box appears.
2. Click the**Van der Waals Calculations** tab.
3. To run the calculation using a cut off technique, un-check **Exact calculation**.
4. Select a cut off technique and set the value of its corresponding parameter.
5. Click **Run**. The output window displays the calculation result.

Energy minimization

When you build your model, the location for each atom may not accurately represent the atom's location in the actual molecule. Your model may depict high-energy strain at various bonds or conformational strain between atoms. As a result, your model may not accurately represent the molecule.

To correct your model, perform an MM2 or MMFF94 energy minimization calculation. When you do, ChemBio3D examines your model and identifies its various atom types. It then calculates a new position of each atom so that the cumulative potential energy for your model is minimized. Having calculated each new position, ChemBio3D moves each atom in your model so that the total energy is at a minimum.

You cannot minimize energy in models containing phosphate groups drawn with double bonds. For information on how to create a model with phosphate groups you can minimize, see the ChemBio3D Drawing FAQ.

Conformation sampling

Stochastic conformation sampling determines likely conformations of a molecule by starting with an initial structure, its atomic coordinates, and its defined bonds.

Each of the atoms' initial X-, Y-, and Z-coordinates are modified by the combination of random numbers to create a new random coordinate position.

The distorted conformation is then minimized using MMFF94 calculations and stored. A new set of random numbers, combined with the atomic coordinates and the steric energy of the new structure, is then calculated.

To perform conformation sampling:

1. Go to **Calculations**>**MMFF94**>**MMFF94 Stochastic Conformation Sampling**. A dialog box appears.

2. Specify the maximum random offset value in nm..
3. Specify the number of conformations to be displayed.
4. Specify the maximum number of steps of minimization.
5. Click **Run**. The result appears in the output window.

Note: *The stochastic method of conformation sampling is not applicable to macromolecules.*

6. To view the conformations, go to **View**>**Model Explorer** and select from the fragment list.

Energy minimization using MMFF94

To perform an MMFF94 minimization:

1. Go to **Calculations**>**MMFF94**>**Perform MMFF94 Minimization.** The Perform MMFF94 Minimization dialog box appears**.**
2. Under Preferences tab in the Perform MMFF94 Minimization dialog box, select any of the following options:

- **Display Every Iteration**- View the model during the calculation (displaying or recording each iteration may increase the calculation time).
- **Copy Measurements to Output Box** -View each measurement in the Output window.
- **Setup new Atom Types before Calculation** - ChemBio3D deletes any custom MMFF94 atom types you have defined for your model. Deselect this option to keep them.
- **Setup new Atom Charges before Calculation** - ChemBio3D replaces custom charges you have entered in the Atom Property table. To retain the custom charges, deselect this option.

3. Click **Run**. The result appears in the output window.

Energy minimization using MM2

To minimize the energy of the molecule based on MM2:

1. Set **Optimal** column measurements in the Measurement table (go to **View**>**Measurement table**).
2. Go to **Calculations**>**MM2**>**Minimize Energy**.
3. In the Minimization Energy dialog box, select any of these options and click **Run:**
   - **Minimum RMS Gradient**-specify the convergence criteria for the gradient of the potential energy surface. Use a large values for shorter calculation time but less accurate results. Use a smaller value for more accurate results but longer calculation time. (The default value of 0.100 is a reasonable compromise).
   - **Display Every Iteration**-view the model during the calculation (displaying each iteration may slow down the calculation).
   - **Copy Measurements to Output Box**-view the value of each measurement in the Output window.
   - **Select Move Only Selected Atoms**-restrict movement of a selected part of a model during the minimization. Calculation results are not affected.

Note: *To interrupt a minimization in progress, click* ***Stop*** *in the* ***Computing*** *dialog box.*

Note: *Before changing MM2 constants, first make a backup copy of the parameter tables.*

📝 ***Note:*** *ChemBio3D 13.0 guesses parameters if you try to minimize a structure containing atom types that MM2 does not support.*

Data for each iteration appears in the Output window when the calculations begin. (However, if you have not selected the **Copy Measurements to Output** option, only the last iteration is displayed).
After the RMS gradient is reduced to less than the requested value, the minimization ends, and the final steric energy components and total appear in the Output window.
Intermediate status messages may appear in the Output window. A message appears if the minimization terminates abnormally (usually caused by a poor starting conformation).
You can perform any action in ChemBio3D that does not move, add, or delete any part of the model. For example, you can move windows during minimization, change settings, or scale your model.

Energy minimization examples
Ethane. Ethane provides a simple example of minimization because it has only one minimum-energy (staggered) and one maximum-energy (eclipsed) conformation.
To minimize energy in ethane:

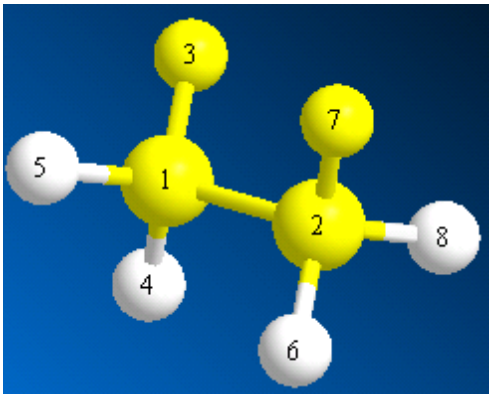
1. (Optional)Go to **View**>**Model Display**>**Display Mode**>**Ball & Stick**.
2. Build a model of ethane in an empty window.
3. (Optional)Go to **View**>**Model Display**>**Show Serial Numbers**.
4. Go to **Calculations**>**MM2**>**Minimize Energy**.
5. Click **Run.**

The calculation results appear in the Output box.
The total steric energy for the conformation is 0.8180 kcal/mol. The 1,4 van der Waals term of 0.6756 dominates the steric energy. This effect is caused by the H-H repulsion contribution.

📝 ***Note:*** *The values of the energy terms shown are approximate and can vary slightly based on the type of processor used to calculate them.*

To view the value of one of the dihedral angles that contributes to the 1,4 van der Waals contribution:

1. Select the atoms making up the dihedral angle as shown in the figure below by SHIFT+clicking **H(7), C(2), C(1),** and **H(4)** in that order.



2. Go to **Structure**>**Measurements**>**Display Dihedral Measurement**.

Figure 6.1: Dihedral measurement for ethane.

The displayed angle represents the lowest energy conformation for the ethane model.
Entering a value in the **Optimal** column imposes a constraint on the minimization routine.
You are increasing the force constant for the torsional term in the steric energy calculation so that you can optimize to the transition state.

1. Select the Rotate tool.
2. Reorient the model by dragging the X- and Y-axis rotation bars until you have an end-on view.

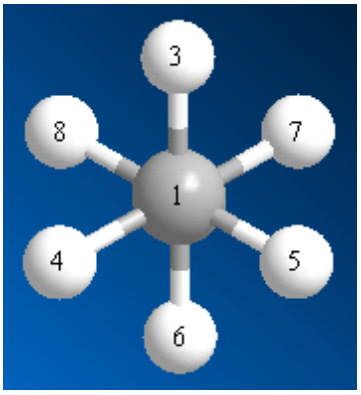


Figure 6.2: Ethane model, end-on view.

To force a minimization to converge on the transition conformation, set the barrier to rotation:

1. In the **Measurement table**, type 0 in the **Optimal** column for the selected dihedral angle and press ENTER.
2. Go to **Calculations**>**MM2**>**Minimize Energy**. The Minimize Energy dialog box appears.

3. Click **Run**.

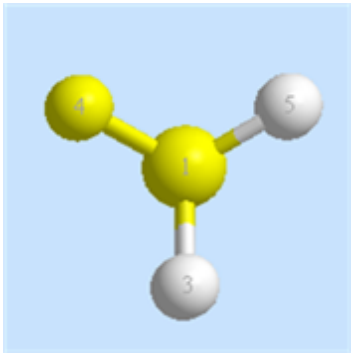


Figure 6.3: Minimized ethane, end-on view.

When the minimization is complete, the model conforms to the eclipsed structure and the reported energy values appear in the Output window. The energy for this eclipsed conformation is higher relative to the staggered form. The majority of the energy contribution is from the torsional energy and the 1,4 van der Waals interactions.

***Note:** The values of the energy terms shown here are approximate and can vary slightly based on the type of processor used to calculate them.*

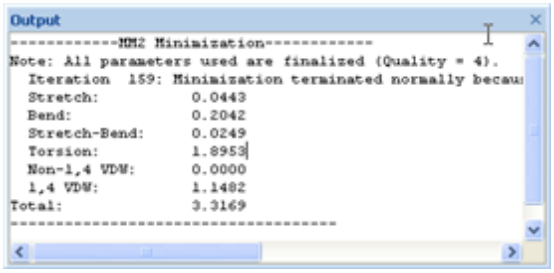


Figure 6.4: Output for eclipsed ethane model.

The dihedral angle in the Actual column becomes 0, corresponding to the imposed constraint.
The difference in energy between the global minimum (Total, previous calculation) and the transition state (Total, this calculation) is 2.50 kcal/mole.
To further illustrate minimization, delete the value from the **Optimal** column for the dihedral angle. Then, click the **MM2** icon on the Calculation toolbar.
After the minimization is complete, the angle is still 0 degrees. This is an important consideration when applying MM2 minimization. It uses first derivatives of energy to determine the next logical move to lower the energy. However, for saddle points (transition states), the region is fairly flat and the minimizer is satisfied that a minimum is reached. If you suspect your starting point is not a minimum, try setting the dihedral angle off by about 2 degrees and minimize again.
Cyclohexane. In this example, you compare the cyclohexane twist-boat conformation and the chair global minimum.
To build a model of cyclohexane:

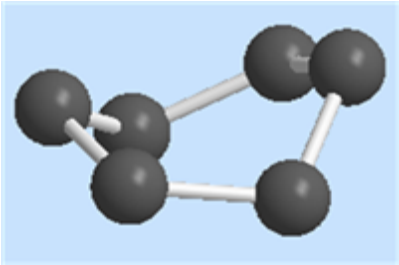
1. Go to **File**>**New**. An empty model window appears.
2. Select the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type CH2(CH2)5 and press ENTER.

Caution: *While there are other, perhaps easier, methods of creating a cyclohexane model, you should use the method described to follow this example.*

Before minimizing, use the **Clean Up Structure** command to refine the model. This generally improves the ability of the Minimize Energy command to reach a minimum point.

1. Go to **Edit**>**Select All**.
2. Go to **Structure**>**Clean Up**.

To perform the minimization, go to **Calculations**>**MM2**>**Minimize Energy** and click **Run**.
When the minimization is complete, reorient the model so it appears as in the figure below.



The conformation you converged to is not the well-known chair conformation, which is the global minimum. Instead, the model has converged on a local minimum, the twisted-boat conformation. This is the closest low-energy conformation to your starting conformation.
Had you built this structure using substructures that are already energy minimized, or in the ChemDraw panel, you would be close to the chair conformation. The minimizer does not surmount the saddle point to locate the global minimum, and the closest minimum is sought.

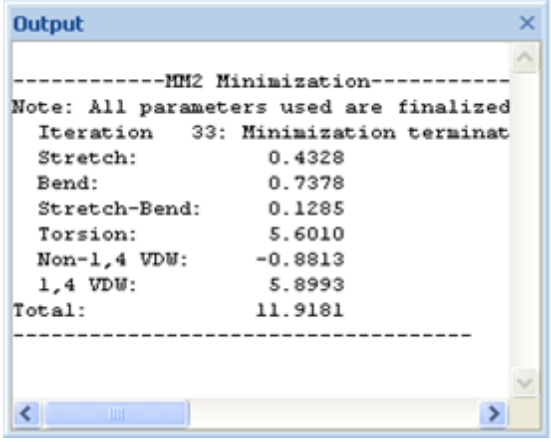


Figure 6.1: Energy values for twisted boat conformation.

The major contributions are from the 1,4 van der Waals and torsional aspects of the model.
For cyclohexane, there are six equivalent local minima (twisted-boat), two equivalent global minima (chair), and many transition states (one of which is the boat conformation).
Finding the global minimum is extremely challenging for all but the most simple molecules. It requires a starting conformation that is already in the valley of the *global* minimum, not in a *local* minimum valley. The case of cyclohexane is straightforward because the global minimum is either of the two possible chair conformations. To obtain the new starting conformation, change the dihedrals of the twisted conformation so that they represent the potential energy valley of the chair conformation.
The most precise way to alter a dihedral angle is to change its Actual value in the Measurement table when dihedral angles are displayed. An easier way to alter an angle, especially when dealing with a ring, is to move the atoms by dragging, then cleaning up the resulting conformation.
To change a dihedral angle:

1. Drag C1 below the plane of the ring. The cursor appears as a box with a hand.
2. Drag C4 above the plane of the ring.

While you drag an atom, the bond lengths and angles become deformed. To return them to the optimal values before minimizing, select the model by dragging a box around it with the Select tool, and run Clean Up.
Now run the minimization:

1. Go to **Calculations**>**MM2**>**Minimize Energy** and click **Run**. Allow the minimization to finish.
2. Reorient the model using the rotation bars to see the final chair conformation.

Note: *The values of the energy terms shown here are approximate and can vary slightly based on the type of processor used to calculate them.*

This conformation is about 5.5 kcal/mole more stable than the twisted-boat conformation.
For molecules more complicated than cyclohexane, where the global minimum is unknown, other methods may be necessary for locating likely starting geometries for minimization. One way of accessing this conformational space of a molecule with large energy barriers is to perform molecular dynamics simulations. This, in effect, heats the molecule, thereby increasing the kinetic energy enough to cross the energetically disfavored transition states.

Molecular dynamics

Molecular Dynamics uses Newtonian mechanics to simulate motion of atoms, adding or subtracting kinetic energy as the molecule's temperature changes.
Molecular Dynamics lets you access the conformational space available to a model by storing iterations of the molecular dynamics run and later examining each frame.
You can perform molecular dynamics simulation using either MM2 or MMFF94.

Molecular dynamics simulation using MMFF94

To perform a molecular dynamics simulation:

1. Build the model (or fragments) to include in the computation.

Note: *The model display type you use affects the speed of the molecular dynamics computation. Model display will decrease the speed in this order: Wire Frame< Sticks < Ball and Sticks< Cylindrical Bonds < Ribbons< Space Fill and van der Waals dot surfaces < Molecular Surfaces.*

2. To view measurements during the simulation, do one of the following:
   - Go to **Structure**>**Measurements**>**Generate All Bond Angles.**
   - Go to **Structure**>**Measurements**>**Generate All Bond Lengths.**
3. In the Measurements table, select the desired measurements.
4. Go to **Calculations**>**MMFF94**>**MMFF94 Molecular Dynamics**. The Molecular Dynamics dialog box appears.
5. Enter the appropriate values:

Step Interval. Specifies the time between simulation steps in femtoseconds (fs). The step interval must be less than ~5% of the vibration period for the highest frequency normal mode, (10 fs for a 3336 cm-1 H–X stretching vibration). Normally a step interval of 1 or 2 fs yields reasonable results. Larger step intervals may cause the integration method to break down, because higher order moments of the position are neglected in the Beeman algorithm.

Frame Interval. Specifies the interval at which frames and statistics are collected. A frame interval of 10 or 20 fs gives a fairly smooth sequence of frames, and a frame interval of 100 fs or more can be used to obtain samples of conformational space over a longer computation.

Terminate After. causes the molecular dynamics run to stop after the specified number of steps. The total time of the run is the Step Interval times the number of steps.

Heating/Cooling Rate. dictates whether temperature adjustments are made. If the Heating/Cooling Rate check box is checked, the Heating/Cooling Rate slider determines the rate at which energy is added to or removed from the model when it is far from the target temperature.

To compute an isoenthalpic trajectory (constant total energy), deselect Heating/Cooling Rate.

Target Temperature. the final temperature to which the calculation will run. Energy is added to or removed from the model when the computed temperature varies more than 3% from the target temperature.

The computed temperature used for this purpose is an exponentially weighted average temperature with a memory half-life of about 20 steps.

6. Click **Run**.

Saving a Job

The job type and settings are saved in a JDF file if you click **Save As** on the dialog box before running a computation. You can then run these computations in a later work session.

Starting the calculation

To begin the computation, click **Run**. The computation begins. Messages for each iteration and measurements you track appear in the Output window. To stop the computation before it finishes, click **Stop** in the **Calculations** toolbar.

Molecular dynamics simulation using MM2

To perform a molecular dynamics simulation:

1. Build the model (or fragments).

Note: *The model display type you use affects the speed of the molecular dynamics computation. Model display will decrease the speed in the following order: Wire Frame < Sticks < Ball and Sticks < Cylindrical Bonds < Ribbons < Space Fill and van der Waals dot surfaces < Molecular Surfaces.*

2. To track a particular measurement during the simulation, select the appropriate atoms and do one of the following:
   - Go to **Structure**>**Measurements**>**Set Bond Angle**
   - Go to **Structure**>**Measurements**>**Set Bond Length**
3. Go to **Calculations**>**MM2**>**molecular Dynamics**. The Molecular Dynamics dialog box appears.
4. Enter the appropriate values.

Step Interval. determines the time between molecular dynamics steps. The step interval must be less than ~5% of the vibration period for the highest frequency normal mode, (10 fs for a 3336 cm-1 H–X stretching vibration). Normally a step interval of 1 or 2 fs yields reasonable results. Larger step intervals may cause the integration method to break down, because higher order moments of the position are neglected in the Beeman algorithm.

Frame Interval. determines the interval at which frames and statistics are collected. A frame interval of 10 or 20 fs gives a fairly smooth sequence of frames, and a frame interval of 100 fs or more can be used to obtain samples of conformational space over a longer computation.

Terminate After. causes the molecular dynamics run to stop after the specified number of steps. The total time of the run is the Step Interval times the number of steps.

Heating/Cooling Rate. dictates whether temperature adjustments are made. If the Heating/Cooling Rate check box is checked, the Heating/Cooling Rate slider determines the rate at which energy is added to or removed from the model when it is far from the target temperature.

A heating/cooling rate of approximately 1.0 kcal/atom/picosecond results in small corrections which minimally disturb the trajectory. A much higher rate quickly heats up the model, but an equilibration or stabilization period is required to yield statistically meaningful results.

To compute an isoenthalpic trajectory (constant total energy), deselect Heating/Cooling Rate.

Target Temperature. indicates the final temperature to which the calculation will run. Energy is added to or removed from the model when the computed temperature varies more than 3% from the target temperature.

The computed temperature used for this purpose is an exponentially weighted average temperature with a memory half-life of about 20 steps.

5. Click **Run**.
6. (Optional) Click Stop to end the computation before it is done.

Saving a Job. The job type and settings are saved in a JDF file if you click **Save As** on the dialog box before running a computation. You can then run these computations in a later work session.

Starting the Calculation. To begin the computation, click **Run**. The computation begins. Messages for each iteration and any measurements you are tracking appear in the Output window. The simulation ends when the number of steps specified is taken. To stop the computation before it is finished, click **Stop** in the **Calculations** toolbar.

Job type settings. Use the Job Type tab to set options for the computation.

Select from these options:

Show Step Information. Report each iteration in the Output box.

Copy Measurements to Output Box. Track a particular measurement.

Move Only Selected Atoms. Restrict movement of a selected part of a model during the minimization.

Save Step Data In. Save a file containing the time (in picoseconds), total energy, potential energy, and temperature data for each step. The word "heating" or "cooling" appears for each step in which heating or cooling was performed. A summary of this data appears in the Message window each time a new frame is created.

The computation begins. Messages for each iteration and measurements appear in the Output window.

The simulation ends when either the number of steps you specify is reached or you stop the computation.

Example. Computing the Molecular Dynamics Trajectory for a Short Segment of Polytetrafluoroethylene (PTFE)

To build the model:

1. Go to **File**>**New**.
2. Select the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type F(C2F4)6F and press ENTER.

A polymer segment comprising six repeat units of tetrafluoroethylene appears in the model window.

To perform the computation:

1. Select C(2), the leftmost terminal carbon, then SHIFT+click C(33), the rightmost terminal carbon.
2. Go to **Structure**>**Measurements**>**Display Distance Measurement**.

A measurement for the overall length of the molecule appears in the Measurement table.

3. Go to **Calculations**>**MM2**>**Molecular Dynamics**.
4. Click **Run**.

When the calculation begins, the Output Window appears:

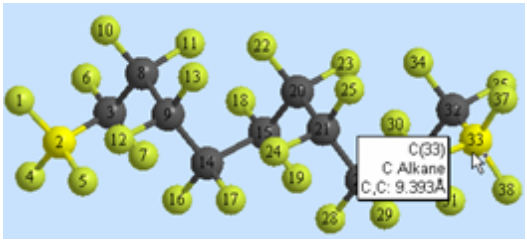


Figure 6.2: C(2) - C(33) distance before calculation.

The C(2)-C(33) distance before the calculation is approximately 9.4Å.

5. Scroll down to the bottom of the Output window and examine the C(2)-C(33) distance for the molecule at 0.190 picoseconds.

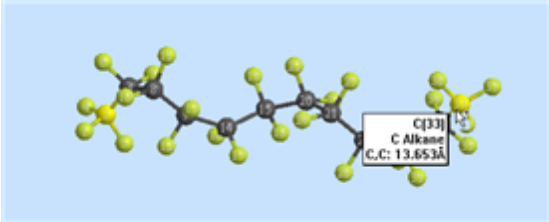


Figure 6.3: C(2) - C(33) distance after calculation.

The C(2)-C(33) distance is approximately 13.7Å, 42% greater than the initial C(2)-C(33) distance.

Gaussian

Gaussian is a command-line driven, computational chemistry application that applies both *ab initio* and semi-empirical methods. It is not included in ChemBio3D but may be purchased from PerkinElmer.

Note: *Gaussian must be installed on the same system on which ChemBio3D is installed.*

ChemBio3D provides an interface for Gaussian calculations. Version 13.0 supports all Gaussian calculations, with these features:

- 13C and 1H NMR spectra predictions
- IR and Raman spectra predictions
- Multi-step jobs
- Partial optimizations
- Support for DFT methods
- Advanced mode

Using Gaussian, ChemBio3D can predict NMR, IR/Raman, and UV/VIS spectra. To calculate a spectrum, go to **Calculations**>**Gaussian Interface** and select the spectrum you want.

Note: *Depending on your computer's speed and memory, and the size of the model, Gaussian calculations may take several minutes.*

Tip: *Run a minimization before predicting spectra. MM2 is faster than Gaussian minimization, and is usually adequate. Gaussian may fail to produce a spectrum if the model is not at a minimum energy state.*

Viewing spectra

To view the predicted spectra, Go to **View**>**Spectrum Viewer**. A a new tab will open in the Spectrum Viewer for each prediction that you run on a given compound.

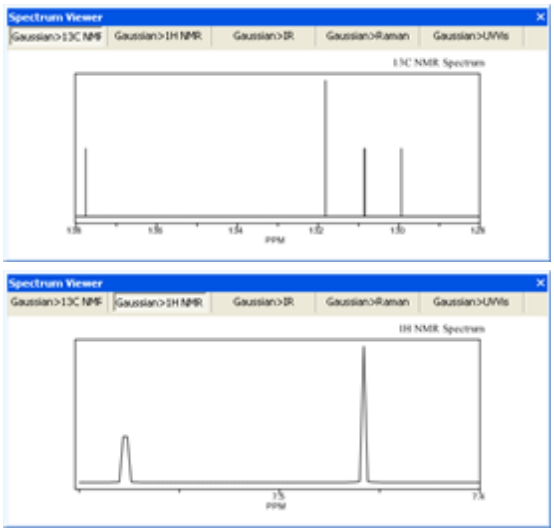


Figure 6.4: Predicted spectra for chlorobenzene.

Tip: *Using the spectrum viewer, you can view spectra produced by computational engines besides Gaussian. See "CS GAMESS" on page 133 for an example.*

Multi-step jobs

You can link jobs and run them with one command. There is no limit to the number of jobs that can be linked. To run multiple jobs:

1. To select your first job (usually Minimization), go to **Calculations**>**Gaussian Interface**, and select the job you want.
2. Click the "**+**" button, and use the Job Type drop-down list to add a new job to the queue.
3. (optional) To remove a job from the queue, select the Link tab and click the "**-**" button.
4. Run the job queue. To terminate the runs at any time, click the stop button on the Calculations toolbar.

Partial optimizations

To perform a partial optimization:

1. Select a part of the model. You may optimize either the selected or unselected portion.
2. Go to **Calculations**>**Gaussian Interface**> **Optimize to Transition state**. In the Gaussian Interface dialog box, in the Coord. System text window, click **Internal Coordinates**.
3. In the Move Which text window, indicate whether the selected or un-selected atoms are to be optimized.
4. Click **Run**.

Note: *If you use Gaussian 09, calculations are done on the Gaussian interface and you need to close the Gaussian 09 interface to view the results in ChemBio3D.*

Input template

Input template is a template file in which certain fields are replaced with variables whose values are to be optimized. The template file is used to construct an actual Gaussian input file containing the current values of the variables for each energy evaluation. The energy is then computed at each step by running a Gaussian fixed point calculation
The General tab of the Gaussian Interface dialog box contains the input template. You can set output parameters with the check boxes and edit keywords in the run file.

Advanced mode

If you are an expert user, you can go directly to a text entry window similar to the input template. Go to **Calculations**>**Gaussian Interface**>**Use Advanced Mode**. Click **Online Gaussian 2003 Keywords** to open the keywords page of the Gaussian Web site.

Optimize to transition state

To optimize your model to a transition state, use a conformation that is as close to the transition state as possible. Do not use a local or global minimum because the algorithm cannot move the geometry from that starting point.
To optimize a transition state:

1. Go to **Calculations**>**Gaussian Interface**>**Optimize to Transition State**. The Gaussian Interface dialog box appears, with Optimize to Transition State as the default Job Type.
2. You can use the defaults or set your own parameters.

   Note: *Unless you are an experienced Gaussian user, use the Transition State defaults.*

3. On the **Properties** tab, select the properties you wish to calculate from the final optimized conformation.
4. On the **General** tab, type any additional keywords that you want to use to modify the optimization.
5. Click **Run**.

Minimizing energy

Minimizing energy is generally the first molecular computation you will perform on a model. You may minimize all or part of a model. To minimize the part of a model, first select the part to include or exclude from the minimization. See "Other Options" on page 107.

1. Go to **Calculations>Gaussian Interface>Minimize (Energy/Geometry**). The Gaussian Interface dialog box appears, with Minimize as the default Job Type.
2. Choose the defaults on the Jobs tab, or set your own parameters.

Following are the different fields available in the Jobs tab.
Job Type. Sets defaults for different types of computations.
Method. Selects a method.
Basis Set. Specifies the basis set. Most methods require a basis set to be specified. See the Gaussian Help file for exceptions.

Wave Function. Selects closed or open shell. See "Specifying electronic configuration" on page 297 for more details.
Polarization. Specifies a polarization function for heavy atoms (P, S, or heavier).
H. If you have selected a Polarization function, choose an H function.
Diffuse. Adds a diffuse function to the basis set. If you use a diffuse function, specify Tight Convergence on the **Advanced** tab. See the Gaussian manual for details.

The **Advanced** tab displays parameters that are adjusted less often. Only those parameters that are applicable to the job type you have selected are active.
For minimizations, the applicable parameters are:
Solvation Model. Selects a solvation model. See the SCRF keyword in the Gaussian manual for information on methods.
Solvent. If you select a solvation model, you may select a solvent. The default solvent for all models is water.
Force Constants. Options are:

- No calculation
- Initial force constants (CalcFC)
- Calculate at each point (CalcAll)

Population Analysis. Options are:

- None—no options
- Full—same as Regular, but for all orbitals
- Minimum—displays the total atomic charges and orbital energies
- Regular — displays five highest occupied and five lowest virtual orbitals, with density matrices and full Mulliken population analysis

Other Options
By default, Gaussian uses modest convergence criteria to speed up calculations. The **Use Tight Convergence Criteria** check box adds the keyword “tight” to the input template to specify full convergence. You may also add a charge by first deselecting the default **Use Formal Charge** check box, or change the **Spin Multiplicity**. Spins can be positive integers. Charges may be plus or minus.
Selecting **Internal Coordinate** lets you minimize only part of the model by choosing either **Selected Atoms** or **Unselected Atoms**.
On the General tab, set the parameters that control the output:
Display Every Iteration. Displays the minimization process “live” at each iteration in the calculation.

📝 ***Note:*** *The Display Every Iteration parameter increases the time to minimize the structure.*

Show Output in Notepad. Sends the output to a text file.
Send Back Output. Displays the value of each measurement in the Output window.

📝 ***Note:*** *The Send Back Output parameter increases the time to minimize the structure.*

Optimize to transition state. To optimize your model to a transition state, use a conformation that is as close to the transition state as possible. Do not use a local or global minimum, because the algorithm cannot effectively move the geometry from that starting point.

Computing properties

To specify the parameters for calculations to predict properties of a model:

1. Go to **Calculations**>**Gaussian**>**Compute Properties**. The Gaussian Interface dialog box appears, with the Properties tab selected.
2. Select the properties to estimate.
3. Click **Run**.

Note: *If you use Gaussian 09, calculations are done on the Gaussian interface and you need to close the Gaussian 09 interface to view the results in ChemBio3D.*

Job description file formats

Job description files are like Preferences files; they store the settings of the dialog box. There are two types as described below.

JDT format. The JDT format is a template from which job types may be derived. The Minimize Energy and Compute Properties job types are read-only examples of these.

JDF format. The JDF format is for saving job descriptions. Click **Save** in the dialog box to save modifications without a warning or confirmation dialog box.

Saving either format within the Gaussian Job folder adds it to the Gaussian submenu for convenient access.

Creating an input file

You can create a Gaussian input file to run. This becomes useful if you want to run the calculation more than once or on a different computer. You must have Gaussian installed to create an input file.

1. Open or create a model.
2. Go to **Calculation**>**Gaussian Interface**>**Create Input File.**
3. Click **Create**.

Running an input file

If you have a previously created GJF Gaussian input file, you can run the file in ChemBio3D.

To run a Gaussian input file:

1. Go to **Calculations > Gaussian Interface>Run Input File**. The Run Gaussian Input file dialog box appears.
2. Type the full path of the Gaussian file or Browse its location.
3. Select the appropriate options.
   a. Show Output in Notepad: Save the output to a file.
   b. Send Back Output: Display the results in the Output window.
4. Click **Run**.

The input file runs. At a certain point, a new tab opens and the model appears in the Model Window.

Running a Gaussian job

ChemBio3D 13.0 lets you select a previously created Gaussian Job Description File (JDF). The JDF file can be thought of as a set of Settings that apply to a particular dialog box.

You can create a JDF file from the dialog box of any of the Gaussian calculations (Minimize Energy, Optimize to Transition State) by clicking **Save As** after all Settings for the calculation have been set. For more information about JDF files see "Job description file formats" on page 108.

To run a Gaussian job:

1. From the **Gaussian** submenu, choose **Run Gaussian Job**. The Open dialog box appears.
2. Select the file to run. The dialog box corresponding to the type of job (Minimize Energy, Compute Properties, and so on.) saved within the file appears.
3. Click **Run**.

Repeating a Gaussian job

After you perform a Gaussian calculation, you can repeat the job as follows:

1. From the **Gaussian** submenu, choose **Repeat** [*name of computation*]. A dialog box appears.
2. Change parameters if desired and click **Run**. The computation proceeds.

CONFLEX

CONFLEX is a conformational analysis package developed by the CONFLEX Corporation. Using CONFLEX, you can search for low energy conformers of a model and create a fragment for each one in its optimal state. To use CONFLEX, ensure that your model consists of only one fragment. Each low energy conformer that CONFLEX finds appears as a separate fragment in the model explorer.

Energy minimization

CONFLEX interface also helps you perform energy minimization of molecules.It supports the following force fields:

- MM2
- MM3
- EMM2
- MMFF
- MMFF94S

To perform energy minimization:

1. Build a model of the structure.
2. Go to **Calculations**>**CONFLEX Interface**>**Minimize (Energy/Geometry)**. The CONFLEX Interface dialog box appears.
3. In the Job & Theory tab, select from these options:
   a. Select the **Energy Potential**.
   b. Select an **Optimization Method**.
   c. Select the **Max Computation Time**.

4. In the General tab, select from these options:
   a. Select a directory in the **Results in** field. The directory is where the calculation results file will be stored.
   b. (Optional) Select a directory in the Backup Calculations Files. A backup file is stored in the location you select.
   c. Select Output files to display in notepad. The files you select will appear in text files after the calculation is complete.
   - INI: This file reports the options you selected in the Job & Theory tab.
   - BSO:This file reports structural and thermodynamic properties of the model.
5. Click **Run**.
6. Click **Yes** in the confirmation box that appears if you want to bring back the minimized molecule in to ChemBio3D.

Note: *If you have opted for the output files to display in notepad in the General tab, you can view the INI file and BSO file as soon as the job is completed.*

Conformation search

To search for conformers:

1. Build a model of the structure.
2. Go to **Calculations**>**CONFLEX Interface**>**Conformation Search**. The CONFLEX Interface dialog box appears.
3. In the Job & Theory tab, select from these options:
   a. Select the **Energy Potential**.
   b. Select an **Optimization Method**.
   c. Select the **Max Computation Time**.
   d. Select the **Conformation Search Limit**.
4. In the General tab, select from these options:
   a. Select a directory in the **Results in** field. The directory is where the calculation results file will be stored.
   b. (Optional) Select a directory in the Backup Calculations Files. A backup file is stored in the location you select.
   c. Select Output files to display in notepad. The files you select will appear in text files after the calculation is complete.
   - INI: This file reports the options you selected in the Job & Theory tab.
   - BSO:This file reports structural and thermodynamic properties of the model.
   - FXO: This file reports structural features of the model and data on the conformations that are found.
5. Click **Run**.

MOPAC

ChemBio3D 13.0 supports CS MOPAC Ultra, a molecular computation application that features several semi-empirical methods.

Note: *Before you install CS MOPAC, you must install ChemBio3D 13.0.*

With CS MOPAC, you can:

- Minimize Energy

- "Optimizing geometry" on page 112
- Optimizing to a Transition State

- Compute properties like:
  - Dipole moment ("Example 1: Dipole moment" on page 120)
  - Cation stability ("Example 2: Cation stability" on page 121)
  - Charge distribution ("Example 3: Charge distribution" on page 122)
  - The polarizability of m-Nitrotoluene ("Example 4: The polarizability of m-Nitrotoluene" on page 123)
  - Phase stability ("Example 5: Phase stability" on page 125)
  - Hyperfine Coupling Constants ("Computing properties" on page 115)
  - UHF spin density ("Example 7: UHF spin density" on page 128)
  - RHF spin density ("Example 8: RHF spin density" on page 129)
- Use CS MOPAC Properties
- Use CS MOPAC files

The procedures assume you have a basic understanding of the computational concepts and terminology of semi-empirical methods, and the concepts involved in geometry optimization (minimization) and fixed-point computations.

Minimizing energy

Minimizing energy is generally the first molecular computation performed on a model. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**. The CS MOPAC Interface dialog box appears, with Minimize as a default Job Type.

Job Type. Sets defaults for different types of computations.

Method. Selects a method.

Wave Function. Selects close or open shell. See "Specifying electronic configuration" on page 297. for more details.

Optimizer. Selects a geometry minimizer. See "Optimizing geometry" on page 112 for more information.

Solvent. Selects a solvent. For more information on solvent effects, see the online MOPAC manual.

Move Which. lets you minimize part of a model by selecting it.

Minimum RMS. Specifies the convergence criteria for the gradient of the potential energy surface. (See also "Gradient norm" on page 116.)

Coord. System. Specifies the coordinate system used for computation.

Use keyword 1SCF. Specifies to do one SCF and then stop

Use keyword MMOK, GEO-OK. Specify Molecular Mechanics correction for amide bonds and also override some safety checks.

Notes

RMS. In an energy minimization routine, the Root Mean Square (RMS) of the derivative of the energy with respect to the Cartesian coordinates is used as a criterion to decide when to stop looking for a lower energy and accept the current value as representing the minimum. In theory, the RMS gradient is zero when an energy minimum has been achieved, however this is not possible to achieve practically. Therefore, a default value for the RMS gradient is set when setting up a geometry optimization.

The default value of 0.100 is a reasonable compromise between accuracy and speed. Reducing the value means that the calculation continues longer as it gets closer to a minimum. Increasing the value shortens the calculation, but leaves you farther from a minimum. Increase the value for a better optimization of a conformation that you know is not a minimum, but you want to isolate it for computing comparative data.
To use a value <0.01, specify LET in the keywords section (General Tab).
Wave Function. Selecting a wave function involves deciding whether to use RHF or UHF computations.

- *RHF* is the default Hartree-Fock method for closed shell systems. To use RHF, select the **Close Shell (Restricted)** wave function.
- *UHF* is an alternative form of the HF method used for open shell systems. To use UHF, select the **Open Shell (Unrestricted)** wave function. To calculate Hyperfine Coupling Constants, select the UHF wave function.

Note: *UHF calculations are typically much slower than RHF calculations.*

Optimizing geometry
ChemBio3D uses the Eigenvector Following (EF) routine as the default geometry optimization routine for minimization calculations. The other alternatives are described below.
TS. The TS optimizer is used to optimize a transition state. It is inserted automatically when you select **Optimize to Transition State** from the **MOPAC Interface** submenu.
BFGS. For large models (over about 500-1,000 atoms) the suggested optimizer is the Broyden-Fletcher-Goldfarb-Shanno procedure. By specifying BFGS, this procedure will be used instead of EF.
LBFGS. For very large systems, the LBFGS optimizer is often the only method that can be used. It is based on the BFGS optimizer, but calculates the inverse Hessian as needed rather than storing it. Because it uses little memory, it is preferred for optimizing very large systems. It is, however, not as efficient as the other optimizers.

Adding keywords
Click the **General** tab to specify additional CS MOPAC keywords. This will tailor a calculation to more exacting requirements. For example, you might use additional keywords to control convergence criteria, to optimize to an excited state instead of the ground state, or to calculate additional properties.

Note: *Other properties that you might specify through the keywords section of the dialog box may affect the outcome. For more information see* *"Using keywords" on page 294**.*

Display Every Iteration	Displays the minimization at each iteration in the calculation. Increases the time to minimize the structure.
Show Output in Notepad	Sends the output to a text file.
Send Back Output	Displays each measurement in the Output window. Increases the time to minimize the structure.

Optimize to transition state. To optimize your model to a transition state, use a conformation that is as close to the transition state as possible. Do not use a local or global minimum, because the algorithm cannot effectively move the geometry from that starting point. See also "Example" on page 114.

To optimize a transition state:

1. Go to **Calculations**>**MOPAC Interface**>**Optimize to Transition State**. The CS MOPAC Interface dialog box appears.
2. On the **Job & Theory** tab select a **Method** and **Wave Function**.

📝 ***Note:*** *Unless you are an experienced CS MOPAC user, use the Transition State defaults.*

3. On the **Properties** tab, select the properties you wish to calculate from the final optimized conformation.
4. On the **General** tab, type any additional keywords to use.
5. Click **Run**. The information about the model and the keywords are sent to CS MOPAC. If you have selected **Send Back Output**, the Output window appears.

The Output window displays the status throughout the minimization.

The table below contains keywords sent to CS MOPAC and some other keywords you can use to affect convergence.

Keyword	Description
EF	Automatically sent to CS MOPAC to specify the use of the Eigenvector Following mini-mizer.
GEO-OK	Automatically sent to CS MOPAC to override checking of the Internal coordinates.
MMOK	Automatically sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.
RMAX=n.nn	The maximum ratio of calculated/predicted energy change. The default is 4.0.
RMIN=n.nn	The minimum ratio of calculated/predicted energy change. The default value is 0.000.
PRECISE	Runs the SCF calculations using a higher precision so that values do not fluctuate from run to run.
LET	Overrides safety checks to make the job run faster (or further).
RECALC=5	Use this keyword if the optimization has trouble converging to a transition state.

For descriptions of error messages reported by CS MOPAC see the MOPAC manual.
To interrupt a minimization in progress, click **Stop**.

Example
This example shows how to locate the eclipsed transition state of ethane.
Build a model of ethane:

1. Go to **File**>**New.**
2. Double-click in the model window. A text box appears.
3. Type CH3CH3 and press ENTER. A model of ethane appears.
4. Select the Rotation tool.
5. Click the arrow next to the Rotation tool, and drag down the Rotation dial.

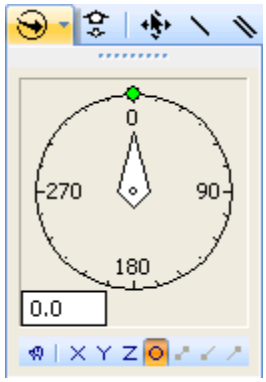


Figure 6.5: The Rotation dial: A) Click here to open the Rotation Dial; B) Dihedral rotators

6. Hold down the S key and select the bond between the C(1) and C(2) atoms.

Note: *Holding down the S key temporarily activates the Select tool.*

7. Select one of the dihedral rotators, then enter 57 in the text box and press ENTER. A nearly eclipsed conformation of ethane is displayed.

Tip: *To view this better, rotate the model on the Y axis until the carbon atoms are aligned.*

Use CS MOPAC to create the precise eclipsed transition state:

1. Holding down the S and SHIFT keys, click any two nearly eclipsed hydrogen atoms, such as H(4) and H(7), to identify the dihedral to track. You should have a nearly coplanar four-atom chain, such as H(4)-C(1)-C(2)-H(7), selected.
2. Go to **Structure**>**Measurements**>**Generate All Dihedral Angles**. The Measurement table appears and displays an actual value for the selected dihedral angle of about 3 degrees (this will vary slightly between experiments).
3. Go to **Calculations**>**MOPAC Interface**>**Optimize to Transition State**.
4. Click **Copy Measurements to Messages** in the **Job Type** tab.
5. Click **Run**. The ethane model minimizes so that the dihedral is 0 degrees, corresponding to the eclipsed conformation of ethane, a known transition state between the staggered minima conformations.

To see the Newman projection of the eclipsed ethane model:

1. Select both carbon atoms.
2. Go to **View**>**View Position**>**Align View Z Axis With Selection**.

Note: *If you perform an Energy Minimization from the same starting dihedral, your model would optimize to the staggered conformation of ethane where the dihedral is 60 degrees, instead of optimizing to the transition state.*

Computing properties

To perform a single point calculation on the current conformation of a model:

1. Go to **Calculations**>**MOPAC Interface**>**Compute Properties.** The Compute Properties dialog box appears.
2. On the **Job & Theory** tab, choose a potential energy function for performing the calculation.
3. On the **Properties** tab:
   a. Select the properties
   b. Select the **charges**
   c. Set the value of Dielectric constant.
4. On the **General** tab, type any additional keywords, if necessary.
5. Click **Run**.

CS MOPAC properties

This section describes the properties that you can calculate for a given conformation of your model, either as a single point energy computation using the Compute Properties command, or after a minimization using either the Minimize Energy or Optimize to Transition State commands.

Heat of formation, ΔH_f. This represents the heat of formation for a model's current conformation. It is useful for comparing the stability of conformations of the same model.

Note: *The heat of formation includes the zero point energies. To obtain the zero point energy for a conformation, run a force operation using the keyword FORCE. The zero-point energy is found at the bottom of the *.out file.*

The heat of formation in CS MOPAC is the gas-phase heat of formation at 298K of one mole of a compound from its elements in their standard state.

The heat of formation comprises these terms:

$$\Delta H_f = E_{elec} + E_{nucl} + E_{isol} + E_{atom}$$

where:

- E_{elec} is calculated from the SCF calculation.
- E_{nucl} is the core-core repulsion based on the nuclei in the molecule.
- E_{isol} and E_{atoms} are parameters supplied by the potential function for the elements within your molecule.

Note: *You can use the keyword ENPART and open the *.out file at the end of a run to view the energy components making up the heat of formation and SCF calculations. See the MOPAC online manual reference, for more information.*

Gradient norm. This is the value of the scalar of the vector of derivatives with respect to the geometric variables flagged for optimization. This property (called GNORM in the MOPAC manual) is automatically selected for a minimization, which calculates the GNORM and compares it to the selected minimum gradient. When the selected minimum is reached, the minimization terminates.

Selecting this property for a Compute Properties operation (where a minimization is not being performed) will give you an idea of how close to optimum geometry the model is for the particular calculation.

Note: *The GNORM property is not the same as the CS MOPAC keyword GNORM. For more information see the MOPAC manual.*

Dipole moment. The dipole moment is the first derivative of the energy with respect to an applied electric field. It measures the asymmetry in the molecular charge distribution and is reported as a vector in three dimensions.

The dipole value will differ when you choose Mulliken Charges, Wang-Ford Charges or Electrostatic Potential, as a different density matrix is used in each computation.

Note: *For more information see the MOPAC manual.*

Charges. This property determines the atomic charges using techniques discussed in the following sections. In this example the charges are the electrostatic potential derived charges from Wang-Ford, because Wang-Ford charges give useful information about chemical stability (reactivity).

Mulliken charges. This property provides a set of charges on an atom basis derived by reworking the density matrix from the SCF calculation. Unlike the Wang-Ford charges used, Mulliken charges give a quick survey of charge distribution in a molecule.

📝 ***Note:*** *For more information, see the MOPAC online manual.*

This contains the keywords sent to CS MOPAC.

Keyword	Description
MULLIK	Sent to CS MOPAC to generate the Mulliken Population Analysis.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.

Electrostatic potential. Electrostatic potential charge computation gives useful information about chemical reactivity.

The electrostatic potential is computed by creating an electrostatic potential grid. ChemBio3D reports the point charges derived from the grid.

In general, these atomic point charges give a better indication of likely sites of attack when compared to atomic charges derived from the Coulson density matrix (Charges) or Mulliken population analysis (Mulliken Charges). The uses for electrostatic potential derived charges are generally the same as for atomic charges. For examples, see "Charges" on page 117.

There are two properties available for calculating atomic point charges: Wang-Ford Charges and Electrostatic Potential.

Wang-Ford charges. This computation of point charges can be used with the AM1 potential function only.

📝 ***Note:*** *For elements not covered by the AM1 potential function, use the Electrostatic Potential property.*

Below are the keywords sent to CS MOPAC.

Keyword	Description
PMEP	Sent to CS MOPAC to specify the generation of Point Charges from PMEP.
QPMEP	Sent to CS MOPAC to specify the Wang/Ford electrostatic Potential routine.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.

Electrostatic potential. Use the electrostatic potential property when the element coverage of the AM1 potential function does not apply to the molecule of interest. For more information see the MOPAC online manual.

This table contains the keywords sent to CS MOPAC and those you can use to affect this property.

Keyword	Description
ESP	Sent to CS MOPAC to specify the Electrostatic Potential routine.
POTWRT	Add this keyword if you want to print out the ESP map values.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.

Molecular surfaces. Molecular surfaces calculate the data to render the Total Charge Density, Molecular Electrostatic Potential, Spin Density, and Molecular Orbitals surfaces.

Polarizability. The polarizability (and hyperpolarizability) provides information about the distribution of electrons based on presence of an applied electric field. In general, molecules with more delocalized electrons have higher polarizability values.

Polarizability data is often used in other equations for optical properties of molecules. For more information see the MOPAC online manual.

The polarizability and hyperpolarizability values reported are the first-order (alpha) tensors (xx, yy, zz, xz, yz, xy), second-order (beta) tensors and third order (gamma) tensors.

📝 ***Note:*** *Polarizabilities cannot be calculated using the MINDO/3 potential function.*

COSMO solvation in water. The COSMO method is useful for determining the stability of various species in a solvent. The default solvent is water. For more information, see the MOPAC online

manual.

To run the COSMO method:

1. Go to **Calculations**>**MOPAC Interface**>**Compute Properties**.
2. On the Job & Theory tab, select COSMO in the **Solvent** field.
3. On the Properties tab, check the **COSMO Area** and/or **COSMO Volume** properties.

Note: *You can also use the Miertus-Scirocco-Tomasi solvation model, which is available using the H2O keyword. This method is recommended only for water as the solvent. A discussion of this method can be found in the CS MOPAC online documentation.*

Hyperfine Coupling Constants. Hyperfine Coupling Constants are useful for simulating Electron Spin Resonance (ESR) spectra.

Hyperfine interaction of the unpaired electron with the central proton and other equivalent protons cause complex splitting patterns in ESR spectra. ESR spectroscopy measures the absorption of microwave radiation by an unpaired electron when it is placed under a strong magnetic field.

Hyperfine Coupling Constants (HFCs) are related to the line spacing within the hyperfine pattern of an ESR spectra and the distance between peaks.

Species that contain unpaired electrons are:

- Free radicals
- Odd electron molecules
- Transition metal complexes
- Rare-earth ions
- Triplet-state molecules

For more information, see the MOPAC online manual.

This table contains the keywords sent to CS MOPAC and those you can use to affect this property.

Keyword	Description
UHF	Sent to CS MOPAC if you choose “Open Shell (Unrestricted)” wave functions to specify the use of the Unrestricted Hartree-Fock methods.
Hyperfine	Sent to CS MOPAC to specify the hyperfine computation.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.

Spin density. Spin density arises in molecules that include an unpaired electron. Spin density data provides relative amounts of alpha spin electrons for a particular state.
Spin density is useful for accessing sites of reactivity and for simulating ESR spectra.
Two methods of calculating spin density of molecules with unpaired electrons are available: RHF Spin Density and UHF Spin Density.
UHF spin density. The UHF Spin Density removes the closed shell restriction. In doing so, separate wave functions for alpha and beta spin electrons are computed. For more information see the MOPAC online manual.
This table contains the keywords sent to CS MOPAC and those you can use to affect this property.

Keyword	Description
UHF	Sent to CS MOPAC if you choose "Open Shell (Unrestricted)" wave functions to specify the use of the Unrestricted Hartree-Fock methods.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.
SPIN	You can add this keyword to print the spin density matrix in the *.out file.

RHF spin density. RHF Spin Density uses the 1/2 electron correction and a single configuration interaction calculation to isolate the alpha spin density in a molecule. This method is useful when the UHF Spin Density computation becomes too resource intensive for large molecules. For more information see the MOPAC online manual.
This table contains the keywords sent to CS MOPAC and those you can use to affect this property.

Keyword	Description
ESR	Sent to CS MOPAC to specify RHF spin density calculation.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.

Example 1: Dipole moment. This example describes how to calculate the dipole moment for formaldehyde:

1. **Go to File>New Model**.
2. Click the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type H2CO and press ENTER. A model of formaldehyde appears.

Figure 6.6: Formaldehyde model.

5. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
6. On the **Theory** tab, choose **AM1**.
7. On the **Properties** tab, select **Dipole**.
8. Click **Run**.

The results shown in the Messages window indicate the electron distribution is skewed in the direction of the oxygen atom.

	X	Y	Z	Total
Dipole (vector Debye)		0.000	0.000	2.317

If you rotate your model, the X,Y, and Z components of the dipole differ. However, the total dipole does not. In this example, the model is oriented so that the significant component of the dipole lies along the X-axis.

Example 2: Cation stability. This example compares cation stabilities in a homologous series of molecules.

To build the model:

1. Go to **File**>**New**.
2. Click the Build from Text tool.
3. Click in the model window. A text box appears.
4. For tri-chloro, type C+Cl3 and press ENTER.
5. Repeat step 1 through step 4 for the other cations: type C+Cl2 for di-chloro; type C+Cl for mono-chloro and CH3+ for methyl cation.

Note: *The cations in this example are even electron closed shell systems and are assumed to have Singlet ground state. No modifications through additional keywords are necessary. The default RHF computation is used.*

To perform the computation:

1. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
2. On the Theory tab, choose **AM1.**
3. On the Properties tab, select **Charges** in the Properties list.

4. Select **Wang-Ford** from the Charges list.
5. Click **Run**. The results for the model appear in the Message window when the computation is complete.

The molecules are now planar, reflecting sp2 hybridization of the central carbon.
From these simple computations, you can reason that the charge of the cation is not localized to the central carbon, but is rather distributed to different extents by MMOK sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.
Example 3: Charge distribution. In this example, we analyze the charge distribution in a series of mono-substituted phenoxy ions.

1. Go to **File**>**New Model**.
2. Click the Build from Text tool.
3. Click in the model window.
4. Type PhO- and press ENTER. A phenoxide ion model appears.

Note: *All the monosubstituted phenols under examination are even electron closed shell systems and are assumed to have Singlet ground state. No modifications by additional keywords are necessary. The default RHF computation is used.*

5. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
6. On the Theory tab, choose **PM3**. This automatically selects **Mulliken** from the Charges list.
7. On the Property tab, select **Charges**.
8. Click **Run**.

To build the para-nitrophenoxide ion:

1. Click the Build from Text tool.
2. Click H10, type NO2, then press ENTER. The para-nitrophenoxide ion displays.

Perform minimization as in the last step.
For the last two monosubstituted nitro phenols, first, select the nitro group using the Select Tool and press DELETE. Add the **nitro group** at the meta (H9) or ortho (H8) position and repeat the analysis.
The data from this series of analyses are shown below. The substitution of a nitro group at para, meta and ortho positions shows a decrease in negative charge at the phenoxy oxygen in the order meta>para>ortho, where ortho substitution shows the greatest reduction of negative charge on the phenoxy oxygen. You can reason from this data that the phenoxy ion is stabilized by nitro substitution at the ortho position.

Phenoxide	p-Nitro	m- Nitro	o-Nitro
C1 0.39572	C1 0.41546	C1 0.38077	C1 0.45789
C2 -0.46113	C2 -0.44929	C2 -0.36594	C2 -0.75764
C3 -0.09388	C3 -0.00519	C3 -0.33658	C3 0.00316
C4 -0.44560	C4 -0.71261	C4 -0.35950	C4 -0.41505
C5 -0.09385	C5 -0.00521	C5 -0.10939	C5 -0.09544
C6 -0.46109	C6 -0.44926	C6 -0.41451	C6 -0.38967
O7 -0.57746	O7 -0.49291	O7 -0.54186	O7 -0.48265
H8 0.16946	H8 0.18718	H8 0.21051	N8 1.38805
H9 0.12069	H9 0.17553	N9 1.31296	H9 0.16911
H10 0.15700	N10 1.38043	H10 0.19979	H10 0.17281
H11 0.12067	H11 0.17561	H11 0.14096	H11 0.13932
H12 0.16946	H12 0.18715	H12 0.17948	H12 0.18090
	O13 -0.70347	O13 -0.65265	O13 -0.71656
	O14 -0.70345	O14 -0.64406	O14 -0.65424

Example 4: The polarizability of *m*-Nitrotoluene. Here is another example of calculating the dipole moment of a model. This time, we use *m*-nitrotoluene:

1. Go to **File**>**New**.
2. Click the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type m-nitrotoluene and press ENTER. A model of m-nitrotoluene appears. Reorient the model using the Rotate tool until it is oriented like the model shown below.

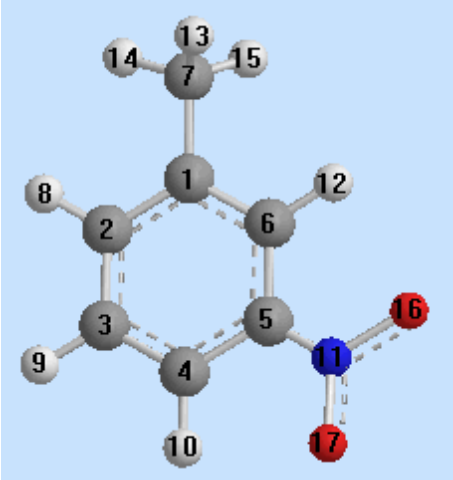


Figure 6.7: m-nitrotoluene model

5. Go to **Edit**>**Select All**.
6. Go to **View**>**Model Display**>**Show Serial Numbers**.
7. With the Build from Text tool, click **H(11)**, then type NO2 in the text box that appears.
8. Press ENTER. A model of *m*-nitrotoluene appears.

Use CS MOPAC to find the dipole moment:

1. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
2. On the Theory tab, choose **AM1**.
3. On the Property tab, select **Polarizabilities**.
4. Click **Run**.

The following table is a subset of the results showing the effect of an applied electric field on the first order polarizability for *m*-nitrotoluene.

Applied field (eV)	alpha xx	alpha yy	alpha zz
0.000000	108.23400	97.70127	18.82380
0.250000	108.40480	97.82726	18.83561
0.500000	108.91847	98.20891	18.86943

The table below contains the keywords sent to CS MOPAC and those you can use to affect this property.

Keyword	Description
POLAR (E=(n1, n2, n3))	Sent to CS MOPAC to specify the polarizablity routine. n is the starting voltage in eV. The default value is E = 1.0. You can reenter the keyword and another value for n to change the starting voltage.
GEO-OK	Sent to CS MOPAC to override checking of the Z-matrix.
MMOK	Sent to CS MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.

Example 5: Phase stability. In this example, we compare the stability of the glycine Zwitterion in water and gas phases.

To compare stabilities:

1. Go to **File**>**New**.
2. Click the Build from Text tool.
3. Click in the model window. A text box appears.
4. Type HGlyOH and press ENTER. A model of glycine appears.

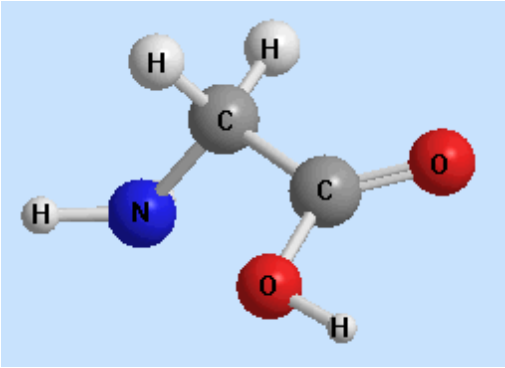


Figure 6.8: Glycine model

5. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
6. On the Job & Theory tab, choose **PM3**.
7. On the Properties tab, click **Heat of Formation, COSMO Area** and **COSMO Volume**.
8. Click **Run**. The results appear in the Messages window.

9. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
10. On the Property tab, deselect **COSMO Area** and **COSMO Volume**.
11. Click **Run**. The results appear in the Messages window.

To create the zwitterion form:

1. Click the Build from Text tool.
2. Click the nitrogen atom , type “+”, then press ENTER.
3. Click the oxygen atom, type “-”, then press ENTER. The glycine zwitterion is formed.

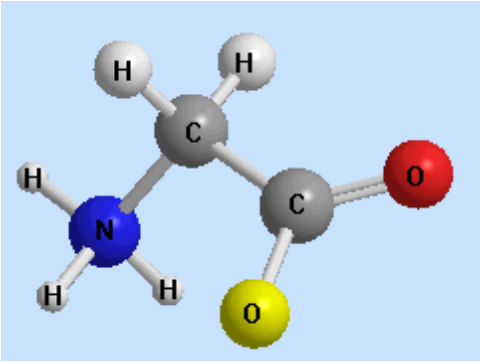


Figure 6.9: Glycine zwitterion

4. Perform a minimization with and without the **COSMO Area** and **COSMO Volume** properties selected as performed for the glycine model.

This table summarizes the results of the four analyses.

Form of glycine	ΔH (kcal/mole)	Solvent Accessible Surface Å^2
neutral (H2O)	-108.32861	52.36067
zwitterion (H2O)	-126.93974	52.37133
neutral (gas)	-92.75386	
zwitterion (gas)	-57.83940	

From this data you can reason that the glycine zwitterion is the more favored conformation in water and the neutral form is more favored in gas phase.

Example 6. This is an example on Hyperfine Coupling Constants and it uses the ethyl radical.

To build the model:

1. Go to **File**>**New Model**.
2. Click the Build from Text tool.

3. Click in the model window. A text box appears.
4. Type EtH and press ENTER.
5. Click the Select tool.
6. Select H(8).
7. Press BACKSPACE to remove the H(8) hydrogen.

If automatic rectification is on, a message appears asking to turn it off to perform this operation.

8. Click **Turn Off Automatic Rectification**. The Ethyl Radical is displayed.

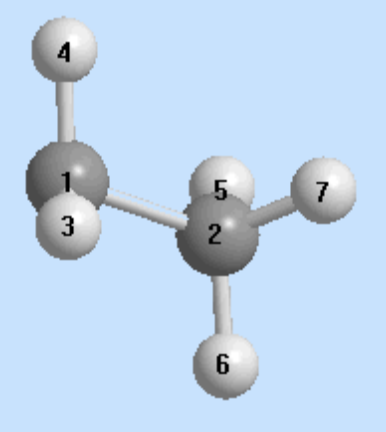


Figure 6.10: Ethyl radical model

To perform the HFC computation:

1. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
2. On the **Job & Theory** tab, choose the **PM3** potential function and the **Open Shell (Unrestricted)** wave function.
3. On the Properties tab, choose **Hyperfine Coupling Constants**.
4. Click **Run**.

This table lists the hyperfine coupling constants.

Hyperfine Coupling Constants	
C1	0.02376
C2	-0.00504
H3	-0.02632
H4	-0.02605
H5	0.00350
H6	0.05672
H7	0.05479

Example 7: UHF spin density. Again, using the ethyl radical, calculate the UHF spin density:

1. Create the ethyl radical as described in "Spin density" on page 120.
2. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
3. On the Theory tab, select **PM3**.
4. On the Properties tab, select **Open Shell (Unrestricted)** and **Spin Density**.
5. Click **Run**.

The Message window displays a list of atomic orbital spin densities.
The atomic orbitals are not labeled for each value, however, the general rule is shown in the table below (CS MOPAC only uses s, p_x, p_y and p_z orbitals).

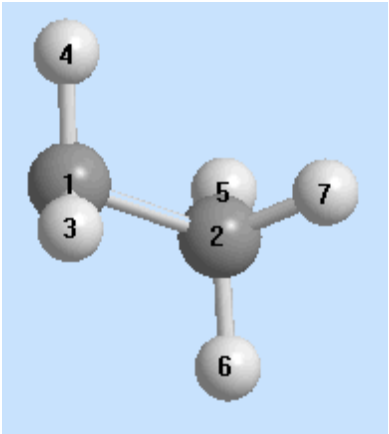
Spin Density	Atomic Orbital.
0.07127	C1 s
0.06739	C1 p_x
0.08375	C1 p_y
0.94768	C1 p_z
-0.01511	C2 S
-0.06345	C2 p_x
-0.01844	C2 p_y

Spin Density	Atomic Orbital.
-0.03463	C2 p_z
-0.07896	H3 s
0.07815	H4 s
0.01046	H5 s
0.05488	H6 s
0.05329	H7 s

You can reason from the result shown that the unpaired electron in the ethyl radical is more localized at p_z orbital on C1. Generally, this is a good indication of the reactive site

Example 8: RHF spin density. This example uses an ethyl radical to calculate the RHF spin density:

1. To create the radical, click in the model window. A text box appears.
2. Type EtH and press ENTER.
3. Click the Select tool.
4. Select H(8).
5. Press **Backspace** to remove the H(8) hydrogen.
   If automatic rectification is on, a message appears asking to turn it off to perform this operation.
6. Click **Turn Off Automatic Rectification**. The Ethyl Radical is displayed.



7. Go to **Calculations**>**MOPAC Interface**>**Minimize Energy**.
8. On the Theory tab, choose **PM3** and **Closed Shell (Restricted)**.
9. On the Properties tab, choose **Spin Density**.
10. Click **Run**.

The Message window displays the total spin densities for each atom (spin densities for all orbitals are totaled for each atom).

📝 ***Note:*** *You can look in the *.out file for a breakdown of the spin densities for each atomic orbital.*

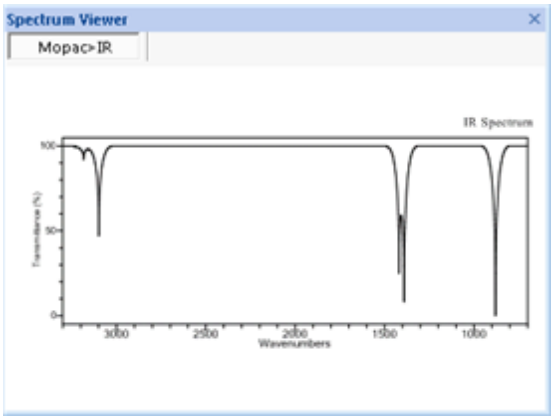
Total Spin Density	Atom
0.90744	C1
0.00644	C2
0.00000	H3
0.00000	H4
0.00001	H5
0.04395	H6
0.04216	H7
0.90744	C1
0.00644	C2
0.00000	H3
0.00000	H4
0.00001	H5
0.04395	H6
0.04216	H7

You can reason from this result that the unpaired electron in the ethyl radical is more localized on C1. Generally, this is a good indication of the reactive site.

Predict IR spectrum

A chart displaying the IR spectrum of the molecule selected can be generated.
To generate the IR spectrum:

1. Go to **Calculations>Mopac interface>Predict IR Spectrum**. The CS MOPAC Interface dialog box appears.
2. On the **Properties** tab, select **Predict IR Spectrum** from Job type list.
3. On the **Job & Theory** tab, set the values of method, wave function, solvent and coordinate system.
4. Click **Run**. The Spectrum viewer displaying the chart appears.



CS MOPAC files

Using output files

Each computation performed using CS MOPAC creates a *.out file that contains all information about the computation. A summary *.arax file is also created, (where x increments from a to z after each run). The *.out file is overwritten for each run, but a new summary *.arax, file is created after each computation (*.araa, *.arab, and so on.)
The OUT and AAX files are saved by default to the **\MOPAC Interface** subfolder in your **My Documents** folder. You may specify a different location from the **General** tab of the CS MOPAC Interface dialog box.This information is found in the summary file for each run:

- Electronic Energy (Eelectronic)
- Core-Core Repulsion Energy (Enuclear)
- Symmetry
- Ionization Potential
- HOMO/LUMO energies

The *.out file contains this information by default.

- Starting atomic coordinates
- Starting internal coordinates
- Molecular orbital energies (eigenvalues)
- Ending atomic coordinates

The workings of many of the calculations can also be printed in the *.out file by specifying the appropriate keywords before running the calculation. For example, specifying the keyword MECI shows the derivation of microstates used in an RHF 1/2 electron approximation. For more information see "Using keywords" on page 294.

Note: *Close the *.out file while performing CS MOPAC computations or the CS MOPAC application stops functioning.*

Input files

A CS MOPAC input file (.MOP) is associated with a model and its dialog box settings.

To create a CS MOPAC input file:

1. Go to **Calculations**>**MOPAC Interface**>**Create Input File**.
2. Select the appropriate settings and click **Create**.

To run an input file:

1. Go to **Calculations**>**MOPAC Interface** and click **Run Input File**. The **Run MOPAC Input File** dialog box appears.
2. Specify the full path of the CS MOPAC file or browse to the file location.
3. Select the appropriate options. For more information about the options, see "Specifying electronic configuration" on page 297.
4. Click **Run**.

A new model window appears displaying the initial model. The CS MOPAC job runs and the results appear.
All properties requested for the job appear in the *.out file. Only iteration messages appear for these jobs.

Note: *If you open a CS MOPAC file that includes a model with an open valence, you can prevent ChemBio3D from readjusting the coordinates by turning off Automatically Rectify in the Building control panel.*

Note: *CS MOPAC input files with multiple instances of the Z-matrix under examination will not be correctly displayed in ChemBio3D. This type of CS MOPAC input files includes calculations that use the SADDLE keyword, or model reaction coordinate geometries.*

Running CS MOPAC jobs

ChemBio3D lets you select a CS MOPAC job description file (JDF). The JDF file can be thought of as a set of Settings that apply to a particular dialog box.
To create a JDF file:

1. Go to **Calculations**>**MOPAC Interface>Create Input File** and choose a calculation.
2. After all settings for the calculation are specified, click **Save As**.

To run a CS MOPAC job from a JDF file:

1. Go to **Calculations**>**MOPAC Interface** and click **Run MOPAC Job**. The Open dialog box appears.
2. Select the JDF file to run. The dialog box corresponding to the type of job saved within the file appears.
3. Click **Run**.

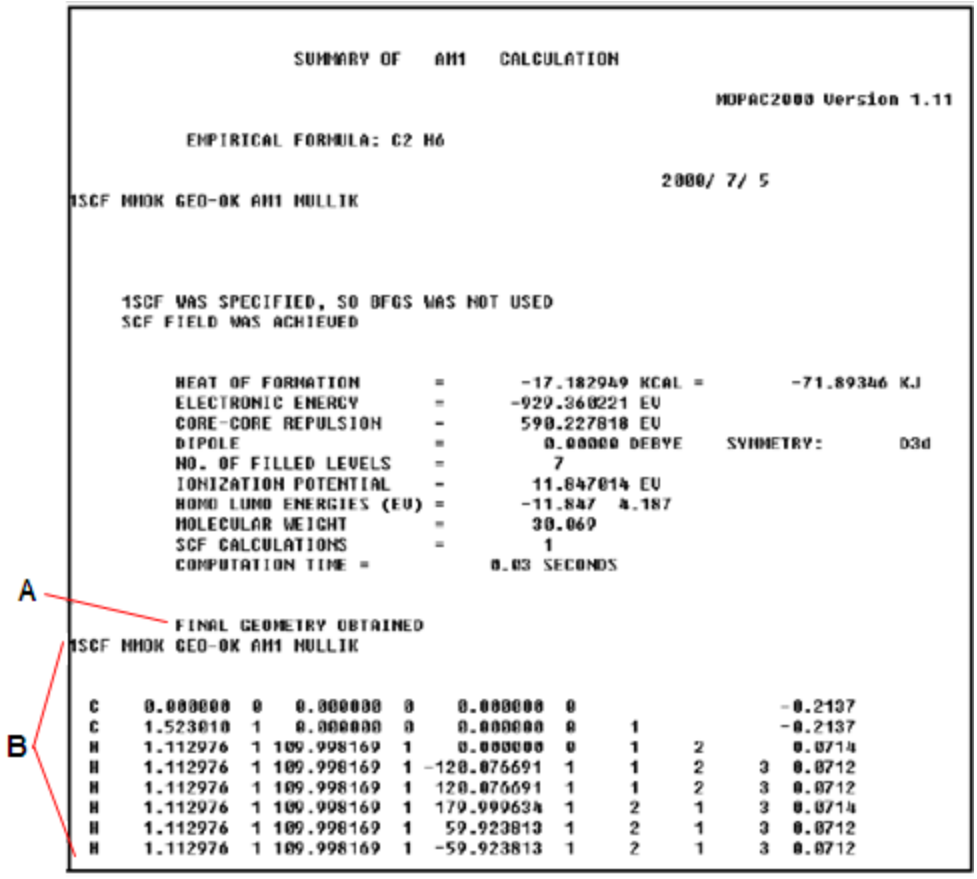
After you perform a CS MOPAC calculation, you can repeat the job as follows:

1. Go to **Calculations**>**MOPAC Interface** and choose **Repeat** [*name of computation*]. The appropriate dialog box appears.
2. Change parameters if desired and click **Run**. The calculation proceeds.

Creating structures from ARC files

When you perform a CS MOPAC calculation, the results are stored in an ARC file in the **\MOPAC Interface** subfolder in your **My Documents** folder.
To create a structure from the ARC file:

1. Open the ARC file in a text editor.
2. Delete the text above the keywords section of the file as shown in this illustration.


SUMMARY OF AM1 CALCULATION
MOPAC2000 Version 1.11
EMPIRICAL FORMULA: C2 H6
2000/ 7/ 5
1SCF MMOK GEO-OK AM1 NULLIK
1SCF WAS SPECIFIED, SO DFGS WAS NOT USED
SCF FIELD WAS ACHIEVED
HEAT OF FORMATION = -17.182949 KCAL = -71.89346 KJ
ELECTRONIC ENERGY = -929.360221 EV
CORE-CORE REPULSION = 590.227818 EV
DIPOLE = 0.00000 DEBYE SYMMETRY: D3d
NO. OF FILLED LEVELS = 7
IONIZATION POTENTIAL = 11.847014 EV
HOMO LUMO ENERGIES (EV) = -11.847 4.187
MOLECULAR WEIGHT = 30.069
SCF CALCULATIONS = 1
COMPUTATION TIME = 0.03 SECONDS
FINAL GEOMETRY OBTAINED
1SCF MMOK GEO-OK AM1 NULLIK
C 0.000000 0 0.000000 0 0.000000 0 -0.2137
C 1.523010 1 0.000000 0 0.000000 0 1 -0.2137
H 1.112976 1 109.998169 1 0.000000 0 1 2 0.0714
H 1.112976 1 109.998169 1 -120.076691 1 1 2 3 0.0712
H 1.112976 1 109.998169 1 120.076691 1 1 2 3 0.0712
H 1.112976 1 109.998169 1 179.999634 1 2 1 3 0.0714
H 1.112976 1 109.998169 1 59.923813 1 2 1 3 0.0712
H 1.112976 1 109.998169 1 -59.923813 1 2 1 3 0.0712
A
B

ARC File: A) Delete text through this line; B) Keyword section

3. Save the file with a MOP extension.
4. Open the MOP file.

CS GAMESS

The General Atomic and Molecular Electronic Structure System (CS GAMESS) is a general *ab initio* quantum chemistry package. It computes wave functions using RHF, ROHF, UHF, GVB, and MCSCF. CI and MP2 energy corrections are available for some of these.

CS GAMESS is installed with ChemBio3D 13.0. CS GAMESS computation features are:

- Minimize Energy
- Optimize to Transition State
- Compute Properties

- Run Frequency
- Predict IR/Raman Spectra
- Predict NMR Spectra

When you choose one of these options, The CS GAMESS interface dialog box appears, with the recommended default parameters for that computation chosen. You may change parameters on any of the tabbed pages of the dialog box before running the computation. If you know what parameter settings you want to use, you can run any computation using any of the options as a starting point. If you are familiar with the CS GAMESS keywords, you can choose **Use Advanced Mode** and get a GUI version of the command line interface.

Viewing spectra

To view the predicted spectra, Go to **View>Spectrum Viewer**. A a new tab will open in the Spectrum Viewer for each prediction that you run on a given compound.

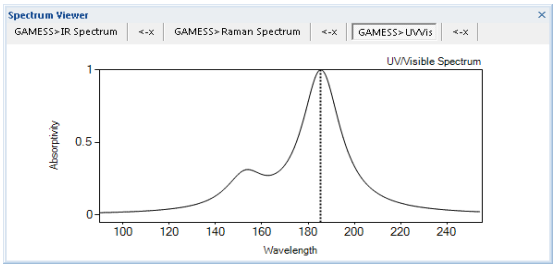


Figure 6.11: Predicting an UV-Vis spectrum for chlorobenzene using GAMESS.

Viewing UV-Vis peaks

Use the UV-Vis Peaks table to view the intensity and position of the peaks in the GAMESS UV-Vis spectrum. To view the table, go to **View>UV-Vis peaks**. Click a row in the table to highlight the corresponding peak in the spectrum.

Tip: *Using the spectrum viewer, you can view spectra produced by computational engines besides GAMESS.*

Minimizing energy

To perform a CS GAMESS Minimize Energy computation on a model:

1. Go to **Calculations>GAMESS>Minimize Energy**. The GAMESS Interface dialog box appears with the **Job & Theory** tab displayed.
2. Use the tabs to customize your computation. See the following sections for details.
3. Click **Run**.

Specifying calculation settings

You can specify the combination of basis set and particular electronic structure theory using the **Job & Theory** tab. By default, the settings on this tab are optimized for *ab initio* computations.

For more detailed information on basis set, see the $BASIS section of the CS GAMESS documentation.

To specify the calculation settings:

1. From the **Method** list, choose a method.
2. From the **Wave Function** list, choose a function.
3. From the **Basis Set** list, choose the basis set.

Note: *To use a Method or Basis Set that is not on the list, type it in the Additional Keywords section on the General tab. For more information, see* *"Specifying electronic configuration" on page 297*.

4. From the **Diffuse** list, select the diffuse function to add to the basis set.
5. Set the **Polarization** functions. If you select a function for Heavy Atom, also select an H option.
6. Select a **Spin Multiplicity** value.
7. Select a **Net Charge** value.

Setting output options

Use the **General** tab to set options for display and recording results of calculations.

To set the job type options:

1. In the Minimize Energy dialog box, click the **Job Type** tab.
2. Select the appropriate options:

Display Every Iteration. Watch the minimization process at each iteration in the calculation.
Displaying or recording each iteration increases the time to minimize the structure

Send output to notepad. Store the output in a notepad file at the specified location

Kill temporary files. Generate only the output file in CS GAMESS interface folder and do not generate the input file

Send Back Output. Display output in the comments box.

Average Equivalent Hydrogens. Aggregate identical protons

Specifying properties to compute

You can specify which properties are computed. The default **Population Analysis** type is Mulliken.

To specify properties:

1. In the Minimize Energy dialog box, click **Properties**.

2. On the **Properties** tab, set these options:
   - Select the properties to calculate
   - Select the Population Analysis type

Specifying the general settings

Use the **General** tab to customize the calculation to the model.

To set the General settings:

1. In the Minimize Energy dialog box, click **General**.
2. On the **General** tab, set these options:
   - Select the Solvation model.

- Type the dielectric constant for the solvent. The box does not appear for gas-phase computations.
- In the **Results In** box, type or browse to the path to the directory where results are stored.
- If desired, add CS GAMESS keywords to the **Additional Keywords** dialog box.

Viewing and animating GAMESS IR vibrations

After you create an infrared spectrum using GAMESS, you can view and animate the IR modes in the Model Window.
To compute the IR spectrum:

1. Draw the structure.
2. Go to **Calculations**>**GAMESS Interface**>**Predict IR/Raman Spectrum**. The GAMESS Interface dialog box opens.
3. In the dialog box, click the **Job & Theory** tab.
4. Click **Run**. The spectrum appears when the computation is done.

Note: *The computation may take several minutes for larger models.*

To animate the IR vibration:

1. Click the IR Spectrum button on the Model Display toolbar. The Animate IR vectors for model dialog box opens.
2. In the dialog box, select either the **Frequency** or the **Intensity** Mode. The drop-down list is sorted by the mode you select.
3. In the drop-down list, select the frequency and intensity to use in the animation (the first number in each number pair is for the mode you chose).
4. Select from these options:
   - **Show Vectors**--display arrows that indicate the direction of the vibration
   - **Displacement**-- control the range of movement of atoms
   - **Speed**-- control the speed of the animation
5. Click **play.**
6. To stop the animation, click **stop**.
7. To return the model to its original starting position, click **reset**.

NMR spectra

You can use GAMESS to predict the ^{13}C and ^{1}H NMR spectra of your model. After ChemBio3D calculates the spectrum, the spectrum appears in the spectrum viewer where you can view, print, or save it. NMR spectra are saved in cdx file format and can be opened in ChemBioDraw.
To view any spectrum that has been calculated, select it at the top of the spectrum viewer.
To create an NMR spectrum:

1. Go to **Calculations**>**GAMESS Interface**>**Predict NMR Spectrum**.
2. In the GAMESS Interface dialog box, select the desired options and click **Run**.

To either save or print the spectrum, right-click in spectrum and select either **Save as** or **Print**.

Saving customized job descriptions

After you customize a job description, you can save it as a Job Description file to use later. For more information, see "Job description file formats" on page 108.

To save a CS GAMESS job:

1. On the **General** tab, type the file name in the **Menu Item Name** text box. The name you choose will appear in the GAMESS menu.
2. Click **Save As**. The Save dialog box appears.
3. Open the folder: \Chem3D\C3D Extensions\GAMESS Job.

Note: *You must save the file in the GAMESS Job folder for it to appear in the menu.*

4. Select the .jdf or .jdt file type.
5. Click **Save**.

Running a CS GAMESS job

You can run an INP GAMESS job files in ChemBio3D.

To run the job file:

1. Go to **Calculations>GAMESS>Run a Job**. The Open dialog box appears.
2. Type the full path of the CS GAMESS file or Browse to location.
3. Click **Open**. The appropriate dialog box appears.
4. Change settings on the tabs if desired.
5. Click **Run.**

Repeating a CS GAMESS job

To repeat a CS GAMESS job:

1. Go to the **Calculations>GAMESS>Repeat** [*name of computation*]. The appropriate dialog box appears.
2. Change parameters if desired and click **Run**.

Parameter Tables

ChemBio3D uses parameter tables for building and analyzing your model. These tables contain energy and topology data for elements, bond types, atom types, and other parameters. Since ChemBio3D uses these tables to build chemically accurate models of actual molecules, you typically will not want to edit the tables. However, the tables are available for expert uses to modify as desired. If you choose to modify the tables, remember that they must be kept in the C3D Items directory.

The parameter tables are:

3-Membered Ring Angles. Bond angles for bonds in 3-membered rings. In force field analysis, angle bending portion of the force field for bonds in 3-membered rings.

4-Membered Ring Angles. Bond angles for bonds in 4-membered rings. In force field analysis, angle bending portion of the force field for bonds in 4-membered rings.

4-Membered Ring Torsionals. The portion of the force field for the torsional angles in your model for atoms in 4-membered rings.

Angle Bending Parameters. Standard bond angles. In force field analysis, the angle bending portion of the force field for bonds.

Bond Stretching Parameters. Standard bond lengths. In force field analysis, bond stretching and electrostatic portions of force field for bonds.

Chem3D Building Atom Types. Building types available for building models.

Conjugated Pisystem Atoms. Bond lengths for bonds involved in pi systems. Pi system portion of the force field for pi atoms.

Conjugated Pisystem Bonds. Pi system portion of the force field for pi bonds.

Electronegativity Adjustments. Adjusts optimal bond length between two atoms when one atom is attached to an atom that is electronegative.

Elements. Contains elements available for building models.

MM2 Atom Type Parameters. van der Waals parameters for computing force field for each atom.

MM2 Atom Types. Atom types in the model that may be used for MM2 calculations.

MM2 Constants. Constants used for computing MM2 force field.

Out-of-Plane Bending Parameters. Parameters to ensure atoms in trigonal planar geometry remain planar. In force field analysis, parameters to ensure atoms in trigonal planar geometry remain planar.

References. Contains information about where parameter information is derived.

Substructures. Contains predrawn substructures for fast model building.

Torsional Parameters. Computes the portion of the force field for the torsional angles in your model.

VDW Interactions. Adjusts specific van der Waals interactions, such as hydrogen bonding.

When you build a model, ChemBio3D 13.0 ensures that the bond lengths and angles in your model meet the criteria specified in the parameter tables.

Applying parameters to a model

To apply parameter tables to your model:

1. Go to **File**>**Model Settings** and select the **Model Building** tab.
2. Select **Apply Standard Measurements**.

Deselect the **Apply Standard Measurements** option to build your model without the constraint of the parameter tables. However, since no parameters are being applied, your model may not be accurate.

Estimated parameters

In certain circumstances, ChemBio3D 13.0 may estimate parameters. For example, during an MM2 analysis, assume a non-MM2 atom type is encountered in your model. Although the atom type is defined in the Atom Types table, the necessary MM2 parameter will not be defined for that atom type. For example, torsional parameters may be missing. This commonly occurs for inorganic complexes, which MM2 does not cover adequately. More parameters exist for organic compounds.
In this case, ChemBio3D makes an educated guess wherever possible. A message indicating an error in your model may appear before you start the analysis. If you ignore the error, you can determine the parameters guessed after the analysis.
To view the parameters used in an MM2 analysis, go to **Calculations**>**MM2**>**Show Used Parameters**. Estimated parameters have a quality value of 1.

Modifying parameter tables

Note: *Adding or changing parameters is not recommended unless you are sure of the information your are adding such as new parameter information documented in journals.*

To add a new parameter to a parameter table:

1. Go to **View**>**Parameter Tables** and choose the parameter table to open.
2. Do one of the following:
   - In the table, right-click a row header and choose **Append Row** from the context menu. A blank row is added to the bottom of the list.
   - Click a row header to select the row, right-click in the selected row, and choose **Insert Row**. A blank row is added above the row you selected.
3. Type the information for the new parameter.
4. Close and save the file.

Note: *Do not duplicate rows in a parameter table. Duplicate parameters to be used in calculations cannot be determined.*

Caution: *The parameter tables are designed to be edited. However, it is strongly recommended that you do not edit the tables unless you are an expert user. Before making changes to any parameters, create a back up copy of the original parameter table and remove it from the C3D Items directory.*

The elements

The Elements table (Elements.xml) contains the elements for building your models. The fields that comprise the Elements table are listed below.

Symbol. Normally you use only the first column of the Elements table while building models. If you are not currently editing a text cell, you can quickly move from one element to another by typing the first letter or letters of the element symbol.

Cov Rad. The covalent radius is used to approximate bond lengths between atoms.

Pattern. The pattern of the element.

Color. The colors of elements are used when the Color by Element check box is selected in the control panel. To change the color of an element, double-click the current color. The Color Picker dialog box appears in which you can specify a new color for the element.

To use an element in a model, type its symbol in the Replacement text box (or paste it, after copying the cell in the "Symbol" field to the Clipboard) and press ENTER when an atom is selected, or double-click an atom. If no atom is selected, a fragment is added.

Atomic number. The atomic number of the element. Atomic numbers are not assigned to either Lone pair elections or generic atoms. Deuterium has an atomic number of 1.2.

Building types

The Building Atom Types table (Chem3D Building Atom Types.xml) contains the atom types used in building models. Normally you use only the first column of the table while building models. To use a building type in a model, type its name in the Replacement text box (or paste it, after copying the name cell to the Clipboard) and press ENTER when an atom is selected, or when you double-click an atom. If no atom is selected, a fragment is added. The fields that comprise a building type record are described below.

Name. The records are ordered alphabetically by atom type name. Building type names must be unique.

Symbol. This field contains the element symbol associated with the building type. The symbol links the Chem3D Building Atom Types table and the Elements table. The element symbol is used in atom labels and when you save files in file formats that do not support building types, such as MDL MolFile.

van der Waals Radius. The van der Waals (van der Waals) radius specifies the size of atom balls and dot surfaces when displaying the Ball & Stick, Cylindrical Bonds or Space Filling models.

When you generate close contacts (go to **Structure**>**Measurements**>**Generate All Close Contacts**), ChemBio3D 13.0 determines close contacts by comparing the distance between pairs of non-bonded atoms to the sum of their van der Waals radii.

Note: *The van der Waals radii specified in the Chem3D Building Atom Types table do not affect the results of an MM2 computation. The radii used in MM2 computations are specified in the MM2 Atom Types table.*

Text. Text numbers determine which measurements apply to a given group of atoms in other parameter tables. For example, C Alkane has a building type number of **1** and O Alcohol has a building type number of **6**. To determine the standard bond length of a bond between a C Alkane atom and an O Alcohol atom, look at the 1-6 record in the Bond Stretching table.

Charge. The charge of a building type is used when assigning building types to atoms in a model. When atom information is displayed, the charge always follows the atom symbol. Charges can be fractional. For example, the charge of a carbon atom in a cyclopentadienyl ring is 0.200.

ChemBio3D displays the formal charge that has been assigned to atoms and calculates the delocalized charge. Both charges are displayed (when applicable) in the popup window when you hover over an atom.

Max Ring. The maximum ring size field indicates whether the corresponding building type should be restricted to atoms found in rings of a certain size. If this cell is zero or empty, then this building type is not restricted. For example, the maximum ring size of C Cyclopropane is 3.

Rectification Type. The rectification type specifies the type of atom used to fill open valences. Rectification atoms are added or deleted as you build your model. To activate rectification, go to **File**>**Model Settings**. On the **Model Building** tab, select the **Rectify** check box.

Possible rectification types are:

D	H
H Alcohol	H Amide
H Amine	H Ammonium
H Carboxyl	H Enol
H Guanidine	H Thiol

When you specify a rectification type, the bound-to type of the rectification type should not conflict with the building type. If there is no rectification type for an atom, it is never rectified.

For example, if the rectification type of O Carboxyl is H Carboxyl, the bound-to type of H Carboxyl should be either O Carboxyl or empty. Otherwise, when assigning building types, hydrogen atoms bound to O Carboxyl atoms are not assigned H Carboxyl.

Geometry. The geometry for a building type describes the number of bonds that extend from this type of atom and the angles formed by those bonds.

These are the possible geometries:

0 Ligand	1 Ligand
5 Ligands	Bent
Linear	Octahedral
Square planar	Tetrahedral
Trigonal bipyramidal	Trigonal planar
Trigonal pyramidal	

Note: *Standard bond angle parameters are used only when the central atom has a tetrahedral, trigonal or bent geometry.*

Double, Triple, and Delocalized Bonds. The number of double, triple, and delocalized bonds are integers ranging from zero to the number of ligands that the geometry specifies. ChemBio3D uses this information both to assign building types based on the bond orders and to assign bond orders based on building types.

Bound to Order. This is the acceptable order of the bond between a building type and the atom type specified in the bound-to type.

For example, for C Carbonyl, only double bonds can be formed to bound-to type O Carboxylate. If there is no bound-to type specified, this field is not used. The possible bound-to bond orders are single, double, triple, and delocalized.

Note: *The bound-to order should be consistent with the number of double, triple, and delocalized bonds for this atom type. If the bound-to type of an atom type is not specified, its bound-to order is ignored.*

Bound to Type. This specifies the building type to which the atom must be bound. If there is no restriction, this field is empty. The Bound-to type is used in conjunction with the Bound-to Order field.

Non-blank Bound-to-Type values:

C Alkene	C Carbocation
C Carbonyl	C Carboxylate
C Cyclopentadienyl	C Cyclopropene
C Epoxy	C Isonitrile
C Metal CO	C Thiocarbonyl
H Alcohol	H Thiol
N Ammonium	N Azide Center
N Azide End	N Isonitrile

N Nitro	O Carbonyl
O Carboxylate	O Epoxy
O Metal CO	O Nitro
O Oxo	O Phosphate
P Phosphate	S Thiocarbonyl

Substructures table

The Substructure table (Substructures.xml) contains a library of substructures for you to use to build models. You can use a substructure as either a template to build a new fragment or to add to an existing model.

To attach a substructure to an existing model:

1. With the Build from Text tool, click an atom in the model.
2. Enter the name of the substructure (see the first column in the Substructrure parameter table) and press ENTER.

To create a new fragment from a substructure:

1. In the Substructure parameter table, right-click the image of the substructure in the Model column and select **Copy** in the context menu.
2. Right-click the model window and select **Paste** in the context window.

Editing the substructure table

To remove a substructure from the table:

1. Click the row number for the substructure you want to remove. The row is highlighted.
2. Right-click a highlighted cell in the row and select **Delete row**. the row is removed.

To add a row to the table:

1. Do one of the following:
   - To add a row before an existing row, right-click the existing row and select **Insert Row**.
   - To add a row at the bottom of the table, right-click any cell and select **Append Row**.
2. In the Name column in the new row, add a name for the substructure.
3. build the subtructure model in the model window.
4. Select the model.
5. Go to **Edit**>**Copy**.
6. In the Substructure table, right-click the Model cell in the new row and select **Paste**.
7. Double-click the Color cell and assign the substructure a color.
8. Close the Substructure window and save your changes when prompted.

References

The References table (References.xml) contains information concerning the source for other parameters. Use of the References table does not affect the other tables.

Two fields are used for each reference record: the reference number and the reference description.

Number. The reference number is an index by which the references are organized. Each measurement also contains a reference field that should contain a reference number, indicating the source for that measurement.

Description. The reference description contains whatever text you want to describe the reference. Journal references or bibliographic data are common examples.

Bond stretching parameters

The Bond Stretching Parameters table (Bond Stretching Parameters.xml) contains information about standard bond lengths between atoms of various atom types. In addition to standard bond lengths is information used in MM2 calculations in ChemBio3D.

The Bond Stretching table contains parameters needed to compute the bond stretching and electrostatic portions of the force field for the bonds in your model.

The Bond Stretching Parameters record consists of these fields: Bond Type, KS, Length, Bond Dpl, Quality, and Reference.

Bond Type. The Bond Type field contains the building type numbers of the two bonded atoms.

For example, Bond Type 1-2 is a bond between an alkane carbon and an alkene carbon.

KS. The KS, or bond stretching force constant field, contains a proportionality constant which directly impacts the strength of a bond between two atoms. The larger the value of KS value, the more difficult it is to compress or to stretch that bond.

Length. The third field, Length, contains the bond length for a particular bond type. The larger the number in the Length field, the longer is that type of bond.

Bond Dpl. The Bond Dpl field contains the bond dipole for a particular bond type. The numbers in this cell indicate the polarity of the bond. A zero value indicates that there is no difference in the electronegativity of the atoms in a particular bond. A positive bond dipole indicates that the building type represented by the first atom type number in the Bond Type field is less electronegative than the building type represented by the second atom type number. Finally, a negative bond dipole means that the building type represented by the first building type number in the Bond Type field is more electronegative than the building type represented by the second atom type number.

For example, the 1-1 bond type has a bond dipole of zero since both alkane carbons in the bond are of the same electronegativity. The 1-6 bond type has a bond dipole of 0.440 since an ether or alcohol oxygen is more electronegative than an alkane carbon.

Finally, the 1-19 bond type has a bond dipole of - 0.600 since a silane silicon is less electronegative than an alkane carbon.

Note: *The 1-5 bond type has a dipole of zero, despite the fact that the carbon and hydrogen atoms on this bond have unequal electronegativity. This approximation drastically reduces the number of dipoles to be computed and has been found to produce acceptable results.*

Angle bending parameters

These parameter tables provide standard bond angle values that ChemBio3D 13.0 uses to determine the angles of bonds between atoms of various atom types. There are three angle bending parameter tables:

Table Name	File Name	Explanation
Angle Bending Parameters	Angle Bending Parameters.xml	Applied when the central atom has four or fewer attachments and the bond angle is not in a three or four membered ring.
3-Membered Ring Angles	3-Membered Ring Angles.xml	Applied in 3-membered rings
4-Membered Ring Angles	4-Membered Ring Angles.xml	Applied in 4-membered rings

ChemBio3D uses additional information to compute the angle bending portions of the MM2 force field for any bond angles in your model that occur in 3- and 4-member rings.

Each of these tables consists of the fields described below:

Angle Type. This field contains the atom type numbers of the three atoms that create the bond angle.

For example, angle type 1-2-1 is a bond angle formed by an alkane carbon bonded to an alkene carbon, which is bonded to another alkane carbon. Notice that the alkene carbon is the central atom of the bond angle.

KB. The KB, or the angle bending constant, contains a measure of the amount of energy required to deform a bond angle described by three atoms. The larger the KB value, the more difficult it is to compress or stretch that bond angle.

–XR2–. This field contains the optimal value of a bond angle where the central atom of that bond angle is not bonded to any hydrogen atoms. X represents the central atom of a bond angle and R represents the non-hydrogen atom bonded to X.

For example, the optimal value of the 1-1-3 angle type for 2,2-dichloropropionic acid is the –XR2– bond angle of 107.8°, since the central carbon (C-2) has no attached hydrogen atoms.

The optimal value of the 1-8-1 angle type for N,N,N-triethylamine is the –XR2– bond angle of 107.7°, because the central nitrogen has no attached hydrogen atoms. Notice that the central nitrogen has a trigonal pyramidal geometry, thus one of the attached non-hydrogen atoms is a lone pair, the other non-hydrogen atom is a carbon.

–XRH–. The –XRH– field contains the optimal value of a bond angle where the central atom of that bond angle is bonded to one hydrogen atom and one non-hydrogen atom. X represents the central atom of a bond angle and R represents the non-hydrogen atom bonded to X and H represents a hydrogen atom bonded to X.

For example, the optimal value of the 1-1-3 angle type for 2-chloropropionic acid is the –XRH– bond angle of 109.9°, since the central carbon (C-2) has one attached hydrogen atom. The optimal value of the 1-8-1 angle type for N,N-

diethylamine is the –XRH– value of 107.7°, because the central N has one attached hydrogen atom. In this case the –XR2– and –XRH– values for the 1-8-1 angle type are identical. As in the N,N,N-triethylamine example above, the only attached non-hydrogen atom is a lone pair.

–XH2–. –XH2– is the optimal value of a bond angle where the central atom of that bond angle is also bonded to two hydrogen atoms.

For example, the optimal value of the 1-1-3 angle type for propionic acid is the –XH2– bond angle of 110.0°, since the central carbon (C-2) has two attached hydrogen atoms.

Conjugated Pisystem bonds

ChemBio3D uses the parameters in the Conjugated Pisystems Bonds table (Conjugated PI System Bonds.xml) to correct lengths and angles of bonds that are part of a pi system. ChemBio3D uses additional information to calculate the pi system portions of the MM2 force field for the pi bonds in a model.

There are five fields in records in the Pi Bonds table: Bond Type, dForce, dLength, Quality, and Reference.

Bond Type. The Bond Type describes the atom type numbers of the two bonded atoms.

For example, bond type 2-2 is a bond between two alkene carbons.

d Force. The dForce is a constant used to decrease the bond stretching force constant of a particular conjugated double bond. The force constant Kx for a bond with a calculated pi bond order x is: $K_x = K_2 - (1 - x) * dForce$

where K_2 is the force constant for a non-conjugated double bond, taken from the Bond Stretching table.

The higher the value of K_x for the bond between two pi atoms, the more difficult it is to compress or stretch that bond.

d Length. The dLength field contains a constant used to increase the bond length of any conjugated double bond. The bond length l_x for a bond with a calculated pi bond order x is:

$l_x = l_2 + (1 - x) * dLength$

where l_2 is the bond length of a non-conjugated double bond, taken from the Bond Stretching table. The higher the value of l_x for the bond between two pi atoms, the longer that bond is.

The quality of a parameter indicates the relative accuracy of the data.

Quality	Accuracy Level
1	The parameter is an estimate by ChemBio3D. See "Estimated parameters" on page 139.
2	The parameter is theorized but not confirmed.
3	The parameter is derived from experimental data.
4	The parameter is well-confirmed.

The reference for a measurement corresponds to a reference number in the References table. References indicate where the parameter data was derived. See the References parameter table for a list of references.

Pi Atoms

The Pi Atoms table (Conjugated Pisystem Atoms.xml) contains the electron property parameters used to correct atoms in pi systems. In ChemBio3D, additional information is used to compute the pi system portions of the MM2 force field for the pi atoms.

The fields in the Pi Atoms table are described below:

Atom Type . The Atom type number field contains the atom type number to which the rest of the Conjugated Pisystem Atoms record applies.

Electron. The Electron field contains the number of electrons that the pi atom contributes to the pi system.

For example, an alkene carbon, atom type number 2, contributes 1 electron to the pi system whereas a pyrrole nitrogen, atom type number 40, contributes 2 electrons to the pi system.

Ionization. The Ionization field contains the amount of energy in electron volts (eV) required to remove a pi electron from an isolated pi atom. The ionization energy increases as the electronegativity of the atom increases.

For example, an alkene carbon has an ionization energy of -11.160 eV, and the more electronegative pyrrole nitrogen has an ionization energy of -13.145 eV.

Repulsion. The Repulsion field is:

- The energy required to keep two electrons, each on separate pi atoms, from moving apart.
- The energy in electron volts (eV) required to keep two electrons, occupying the same orbital on the same pi atom, from moving apart.

The repulsion energy increases as the electronegativity of the atom increases. For example, an alkene carbon has an repulsion energy of 11.134 eV, and the more electronegative pyrrole nitrogen has an repulsion energy of 17.210 eV.

The quality of a parameter indicates the relative accuracy of the data.

Quality	Accuracy Level
1	The parameter is an estimate by ChemBio3D. See "Estimated parameters" on page 139.
2	The parameter is theorized but not confirmed.
3	The parameter is derived from experimental data.
4	The parameter is well-confirmed.

The reference for a measurement corresponds to a reference number in the References table. References indicate where the parameter data was derived. See the References parameter table for a list of references.

Electronegativity adjustments

ChemBio3D uses the parameters in the Electronegativity Adjustments table (Electronegativity Adjustments.xml) to adjust the optimal bond length between two atoms when one of the atoms is attached to a third atom that is

electronegative. For example, the carbon-carbon single bond length in ethane is different from that in ethanol. The MM2 parameter set has one parameter for carbon-carbon single bond lengths (1.523Å). The electronegativity correction parameters allow the C-C bond in ethanol to be corrected. The electronegativity parameter used in the Electronegativity Corrections table is the 1-1-6 angle type, where atom type 1 is a C Alkane and atom type 6 is an O Alcohol. The value of this parameter is -0.009Å. Thus the C-C bond length in ethanol is 0.009Å shorter than the standard C-C bond length.

MM2 constants

The MM2 Constants table (MM2 Constants.xml) contains parameters that ChemBio3D uses to compute the MM2 force field.

Cubic and Quartic Stretch Constants. Integrating the Hooke's Law equation provides the Hooke's Law potential function, which describes the potential energy of the ball and spring model. The shape of this potential function is the classical potential well.

$$-\frac{dV}{dx} = F = -dx$$

The Hooke's Law potential function is quadratic, thus the potential well created is symmetrical. The real shape of the potential well is asymmetric and is defined by the Morse Function, but the Hooke's Law potential function works well for most molecules.

$$V(x) = \oint_0^x dV = k\oint_0^x x dx = \frac{1}{2}kx^2$$

Certain molecules contain long bonds which are not described well by Hooke's Law. For this reason the MM2 force field contains a cubic stretch term. The cubic stretch term allows for an asymmetric shape of the potential well, thereby allowing these long bonds to be handled. However, the cubic stretch term is not sufficient to handle abnormally long bonds. Thus the MM2 force field contains a quartic stretch term to correct for problems caused by these abnormally long bonds.

Type 2 (-CHR-) Bending Force Parameters for C-C-C Angles.

- -CHR- Bending K for 1-1-1 angles
- -CHR- Bending K for 1-1-1 angles in 4-membered rings
- -CHR- Bending K for 22-22-22 angles in 3-membered rings

These constants are distinct from the force constants specified in the Angle Bending table. The bending force constant (K) for the 1-1-1 angle (1 is the atom type number for the C Alkane atom type) listed in the MM2 Angle Bending parameters table is for an alkane carbon with two non-hydrogen groups attached. Angle bending parameters for carbons with one or two attached hydrogens differ from those for carbons with no attached hydrogens. Because carbons with one or two attached hydrogens frequently occur, separate force constants are used for these bond angles.

The -CHR- Bending K for 1-1-1 angles allows more accurate force constants to be specified for the Type 1 (-CH2-) and Type 2 (-CHR-) interactions. In addition, the -CHR- Bending K for 1-1-1 angles in 4-membered rings and the -CHR- Bending K for 22-22-22 angles (22 is the atom type number for the C Cyclopropane atom type) in 3-membered rings differ from the aforementioned -CHR- Bending K for 1-1-1 angles and thus require separate constants to be accurately specified.

Stretch-Bend Parameters.

- X-B,C,N,O-Y Stretch-Bend interaction force constant
- X-B,C,N,O-H Stretch-Bend interaction force constant
- X-Al,S-Y Stretch-Bend force constant
- X-Al,S-H Stretch-Bend force constant
- X-Si,P-Y Stretch-Bend force constant
- X-Si,P-H Stretch-Bend force constant
- X-Ga,Ge,As,Se-Y Stretch-Bend force constant

The stretch-bend parameters are force constants for the stretch-bend interaction terms in the prior list of elements. X and Y represent any non-hydrogen atom.

When an angle is compressed, the MM2 force field uses the stretch-bend force constants to lengthen the bonds from the central atom in the angle to the other two atoms in the angle.

For example, the normal C-C-C bond angle in cyclobutane is 88.0°, as compared to a C-C-C bond angle of 110.8° in cyclohexane. The stretch-bend force constants are used to lengthen the C-C bonds in cyclobutane to 1.550Å, from a C-C bond length of 1.536Å in cyclohexane.

Sextic Bending Constant. Sextic bending constant (* 10**8)

ChemBio3D uses the sextic bending constant to increase the energy of angles with large deformations from their ideal value.

Dielectric Constants.

- Dielectric constant for charges
- Dielectric constant for dipoles

The dielectric constants perform as inverse proportionality constants in the electrostatic energy terms. The constants for the charge and dipole terms are supplied separately so that either can be partially or completely suppressed.

The charge-dipole interaction uses the geometric mean of the charge and dipole dielectric constants.

For example, when you increase the Dielectric constant for dipoles, a decrease in the Dipole/Dipole energy occurs. This has the effect of reducing the contribution of dipole-dipole interactions to the total steric energy of a molecule.

Electrostatic and van der Waals cutoff parameters. These parameters define the minimum distance at which the fifth-order polynomial switching function is used for the computation of the listed interactions.

- Cutoff distance for charge/charge interactions Cutoff distance for charge/dipole interactions
- Cutoff distance for dipole/dipole interactions
- Cutoff distance for van der Waals interactions

MM2 atom type parameters

The MM2 Atom Types table (MM2 Atom Types.xml) contains the van der Waals parameters used to compute the force field for each atom in your model.

Each MM2 Atom Type record contains eight fields: Atom type number, R*, Eps, Reduct, Atomic Weight, Lone Pairs, Quality, and Reference.

Text type number

The Text number field is the atom type to which the rest of the MM2 Atom Type Parameter record applies. The records in the MM2 Atom Type table window are sorted in ascending order of Atom Type Atom type number.

R. The R field is the van der Waals radius of the particular atom. The larger the van der Waals radius of an atom is, the larger that atom.

Note: *ChemBio3D uses the van der Waals radius, R, in the MM2 Atom Types table for computation. It is not the same as the van der Waals radius in the Atom Types table, which is used for displaying the model.*

Eps. The Eps or Epsilon field is a constant that is proportional to the depth of the potential well. As the value of epsilon increases, the depth of the potential well increases, as does the strength of the repulsive and attractive interactions between an atom and other atoms.

Note: *For specific van der Waals interactions, the R and Eps values from the van der Waals Interactions table are used instead of values in the MM2 Atom Types table. See "van der Waals Interactions" for more information.*

Reduct. Reduct is a constant used to position the center of the electron cloud on a hydrogen atom toward the nucleus of the carbon atom to which it is bonded by approximately 10% of the distance between the two atoms.

Any atom in a van der Waals potential function must possess a spherical electron cloud centered about its nucleus. For most larger atoms this is a reasonable assumption, but for smaller atoms such as hydrogen it is not. Molecular mechanics calculations based on spherical electron clouds centered about hydrogen nuclei do not give accurate results.

However, it is a reasonable compromise to assume that the electron cloud about hydrogen is still spherical, but that it is no longer centered on the hydrogen nucleus. The Reduct constant is multiplied by the normal bond length to give a new bond length which represents the center of the repositioned electron cloud.

The value of the Reduct field for all non-hydrogen atoms is zero.

Atomic weight. The fifth field, Atomic Weight, is the atomic weight of atoms represented by this atom type number.

Note: *The atomic weight is for the isotopically pure element. For example, the atomic weight for atom type number 1 is 12.000, the atomic weight of* ^{12}C.

Lone pairs. The Lone Pairs field contains the number of lone pairs around a particular atom type. Notice that an amine nitrogen, atom type number 8, has one lone pair and an ether oxygen, atom type number 6, has two lone pairs. Lone pairs are treated explicitly for atoms such as these, which have distinctly non-spherical electron distributions. For atom types such as O Carbonyl, which have more nearly spherical electron distributions, no explicit lone pairs are necessary.

📝 ***Note:*** *Lone pairs are not automatically displayed in atoms that require them.*

Torsional parameters

The Torsional Parameters table (Torsional Parameters.xml) contains parameters used to compute the portions of the MM2 force field for the torsional angles in your model. The 4-Membered Ring Torsional Parameters (4-membered Ring Torsionals.xml) contains torsional parameters for atoms in 4-membered rings.

Each record in the Torsional Parameters table and the 4-Membered Ring Torsional Parameters table consists of six fields: Dihedral Type, V1, V2, V3, Quality, and Reference.

Dihedral Type

The Dihedral Type field contains the atom type numbers of the four atom types that describe the dihedral angle.

For example, angle type 1-2-2-1 is a dihedral angle formed by an alkane carbon bonded to an alkene carbon that is bonded to a second alkene carbon which, in turn, is bonded to another alkane carbon. In other words, angle type 1-2-2-1 is the dihedral angle between the two methyl groups of 2-butene.

The two alkene carbons are the central atoms of the dihedral angle.

V1

The V1, or 360° Periodicity Torsional constant, field contains the first of three principal torsional constants used to compute the total torsional energy in a molecule. V1 derives its name from the fact that a torsional constant of 360° periodicity can have only one torsional energy minimum and one torsional energy maximum within a 360° period. The period starts at -180° and ends at 180°.

A positive value of V1 means that a maximum occurs at 0° and a minimum occurs at ±180° in a 360° period. A negative value of V1 means that a minimum occurs at 0° and a maximum occurs at ±180° in a 360° period. The significance of V1 is explained in the example following the V2 discussion.

V2

The V2, or 180° Periodicity Torsional constant, field contains the second of three principal torsional constants used to compute the total torsional energy in a molecule. V2 derives its name from the fact that a torsional constant of 180° periodicity can have only two torsional energy minima and two torsional energy maxima within a 360° period.

A positive value of V2 indicates there are minima at 0° and +180°, and there are maxima at -90° and +90° in a 360° period. A negative value of V2 causes the position of the maxima and minima to be switched, as in the case of V1 above.

A good example of the significance of the V1 and V2 torsional constants exists in the 1-2-2-1 torsional parameter of 2-butene. The values of V1 and V2 in the Torsional Parameters table are -0.100 and 10.000 respectively.

Because a positive value of V2 indicates that there are minima at 0° and +180°, these minima signify cis-2-butene and trans-2-butene respectively. Notice that V2 for torsional parameters involving torsions about carbon-carbon double bonds all have values ranging from approximately V2=8.000 to V2=16.250. In addition, V2 torsional parameters involving torsions about carbon-carbon single bonds all have values ranging from approximately V2=-2.000 to V2=0.950.

The values of V2 for torsions about carbon-carbon double bonds are higher than those values for torsions about carbon-carbon single bonds. A consequence of this difference in V2 values is that the energy barrier for rotations about double bonds is much higher than the barrier for rotations about single bonds.
The V1 torsional constant creates a torsional energy difference between the conformations represented by the two torsional energy minima of the V2 constant. As discussed previously, a negative value of V1 means that a torsional energy minimum occurs at 0° and a torsional energy maximum occurs at 180°. The value of V1=-0.100 means that cis-2-butene is a torsional energy minimum that is 0.100 kcal/mole lower in energy than the torsional energy maximum represented by trans-2-butene.
The counterintuitive fact that the V1 field is negative can be understood by remembering that only the total energy can be compared to experimental results. In fact, the total energy of trans-2-butene is computed to be 1.423 kcal/mole lower than the total energy of cis-2-butene. This corresponds closely with experimental results. The negative V1 term has been introduced to compensate for an overestimation of the energy difference based solely on van der Waals repulsion between the methyl groups and hydrogens on opposite ends of the double bond. This example illustrates an important lesson:
There is not necessarily any correspondence between the value of a particular parameter used in MM2 calculations and value of a particular physical property of a molecule.

V3

The V3, or 120° Periodicity Torsional constant, field contains the third of three principal torsional constants used to compute the total torsional energy in a molecule. V3 derives its name from the fact that a torsional constant of 120° periodicity can have three torsional energy minima and three torsional energy maxima within a 360° period. A positive value of V3 indicates there are minima at -60°, +60° and +180° and there are maxima at -120°, 0°, and +120° in a 360° period. A negative value of V3 causes the position of the maxima and minima to be reversed, as in the case of V1 and V2 above. The significance of V3 is explained in the following example.
The 1-1-1-1 torsional parameter of n-butane is an example of the V3 torsional constant. The values of V1, V2 and V3 in the Torsional Parameters table are 0.200, 0.270 and 0.093 respectively. Because a positive value of V3 indicates that there are minima at -60°, +60° and +180° and there are maxima at -120°, 0°, and +120°, the minima at ±60° signify the two conformations of n-butane in which the methyl groups are gauche to one another. The +180° minimum represents the conformation in which the methyl groups are anti to one another. The maximum at 0° represents the conformation in which the methyl groups are eclipsed. The maxima at ±120° conform n-butane in which a methyl group and a hydrogen are eclipsed.
The V1 and V2 torsional constants in this example affect the torsional energy in a similar way to the V1 torsional constant for torsions about a carbon-carbon double bond (see previous example).

Note: *The results of MM2 calculations on hydrocarbons do not correspond well with the experimental data on hydrocarbons when only the V3 torsional constant is used (when V1 and V2 are set to zero). However, including small values for the V1 and V2 torsional constants in the MM2 calculations for hydrocarbons dramatically improve the correspondence of the MM2 results with experimental results. This use of V1 and V2 provides little correspondence to any particular physical property of hydrocarbons.*

Out-of-plane bending

The Out-of-Plane Bending table (Out-of-Plane Bending Parameters.xml) contains parameters that ensure that atoms with trigonal planar geometry remain planar in MM2 calculations. The table contains four fields: Bond Type, Force Constant, Quality and Reference.

Bond Type

The first field is the Bond Type, which is described by the atom type numbers of the two bonded atoms.
For example, Bond Type 2-3 is a bond between an alkene carbon and a carbonyl carbon.

Force constant

The force constant field, or the out-of-plane bending constant field, indicates the amount of energy required to cause a trigonal planar atom to become non-planar. The larger the value of the force constant for an atom, the more difficult it is to coerce that atom to be non-planar.

Note: *Out-of-plane bending parameters are not symmetrical. For example, the force constant for a 2-3 bond refers to the plane about the type 2 atom. The force constant for a 3-2 bond refers to the plane about the type 3 atom.*

Qualty

The quality of a parameter indicates the relative accuracy of the data.

Quality	Accuracy Level
1	The parameter is an estimate by ChemBio3D. See "Estimated parameters" on page 139.
2	The parameter is theorized but not confirmed.
3	The parameter is derived from experimental data.
4	The parameter is well-confirmed.

Reference

The reference for a measurement corresponds to a reference number in the References table. References indicate where the parameter data was derived. See the References parameter table for a list of references.

van der Waals interactions

The parameters contained in the van der Waals parameters table (van der Waals Interaction.xml) are used to adjust specific van der Waals interactions in a molecule, such as hydrogen bonding, to provide better correspondence with experimental data in calculating the MM2 force field.

For example, consider the van der Waals interaction between an alkane carbon (Atom Type 1) and a hydrogen (Atom Type 5). Normally, the van der Waals energy is based on the sum of the van der Waals radii for these atoms, found for each atom in the Atom Types table (1.900Å for Atom type number 1 + 1.400Å for Atom type number 2 = 3.400Å). However, better correspondence between the computed van der Waals energy and experimental data is found by substituting this sum with the value found in the van der Waals Interactions table for this specific atom type pair (Atom Types 1-5 = 3.340Å). Similarly, an Eps parameter is substituted for the geometric mean of the Eps parameters for a pair of atoms if their atom types appear in the van der Waals Interactions table.

Docking

Docking helps you determine how a small molecule (a ligand) may be arranged to fit inside a cavity in a larger molecule (a receptor) in energetically favorable orientations. For example, you can explore possible conformers of a drug candidate to determine whether it can attach to a binding site in a selected protein.
ChemBio3D maintains an interface to AutoDock to perform the docking calculation. AutoDock starts with a random population of *poses* of the ligand. A pose is an instance of the ligand at a given orientation, location, and conformation. AutoDock selects the best poses from the population and discards the rest. From the selection, AutoDock develops new poses to rebuild the population using a genetic algorithm[1] . Each selection/rebuilding cycle is a *generation*. AutoDock repeats the cycle for a maximum number of generations that you define. From the final generation, AutoDock retrieves the best poses and reports them as the final calculation results.

Note: *AutoDock functions generate a log file. If AutoDock reports an error, refer to the log file to determine whether the error is the result of an AutoDock or a ChemBio3D function. See* *"Technical Support" on page 1**.*

Installing AutoDock

Before using AutoDock, you must install both AutoDock and AutoDockTools. It is available from the AutoDock Web site as a free download. You need to install it only once.
To install AutoDock:

1. In ChemBio3D 13.0, go to **Calculations**>**AutoDock Interface**>**Install AutoDock/AutoDock Tools**.
2. In the AutoDock dialog box, click **Download AutoDock**. The AutoDock Web site opens in a Web browser, displaying the download instructions.
3. Download and install AutoDock 4 to your local hard drive.

   Note: *Ensure that you download AutoDock 4 and not AutoDock Vina.*

4. In the AutoDock dialog box, click **Set AutoDock Path** to select the path to where you installed AutoDock.

Installing AutoDock Tools

Like AutoDock, the AutoDock tools are free to install. You need to install the tools only once.
To install the AutoDock tools:

1. In ChemBio3D 13.0, go to **Calculations**>**AutoDock Interface**>**Install AutoDock/AutoDock Tools**.
2. In the AutoDock dialog box, click **Download AutoDock Tools**. The AutoDock Web site opens in a Web browser, displaying the download instructions.
3. Download and install AutoDock Tools to your local hard drive.

[1]For more information, see the AutoDock User Guide.

Note: *You do not need to accept or install the packages listed at the end of the installation. They are unnecessary for using the AutoDock tools.*

4. In the AutoDock dialog box, click **Set AutoDockTools Path** to select the path to where you installed the AutoDock tools.

Configuring AutoDock

When you download AutoDock and the AutoDock Tools, you indicate where in your local drive you want to store the files. You can move these files to another directory or download them again as needed. You can also change where AutoDock stores the generated log files.

To configure AutoDock:

1. If the AutoDock Interface is not open, go to **Calculations**>**AutoDock Interface**>**Setup AutoDock Calculation**.
2. Select the General tab.
3. To change the AutoDock working folder, click **Change Directory** under Working Directory. This folder contains all the temporary files used in the current AutoDock run.
   a. Browse for a new folder to save the log files, and click **OK**.

Note: *You will not be permitted with the calculation unless the working directory is empty of files. You have to either choose another directory using* ***Change Directory*** *option, or browse to the working directory and delete the files.*

4. (Optional)To change the AutoDock files folder, click **Change Directory** under AutoDock. This folder contains the AutoDock executable files. This location should only be changed if the location of the AutoDock executable file changes.
   a. Browse for a new folder to save the AutoDock files, and click **OK**.
5. (Optional)To change the AutoDock Tool files folder, click **Change Directory** under AutoDock Tools. This folder contains the AutoDock tools executable files. This location should only be changed if the location of the AutoDock tools executable file changes.
   a. Browse for a new folder to save the AutoDock Tools files, and click **OK**.
6. (Optional) To install AutoDock:
   a. In the AutoDock dialog box, click **Download AutoDock**. The AutoDock download instructions appear in a Web browser.
   b. Download and install the latest version of AutoDock to your local hard drive.
   c. In the AutoDock dialog box, click **Set AutoDock Directory** to select the path to where you installed AutoDock.
7. (Optional)To install the AutoDock Tools:
   a. In the AutoDock dialog box, click **Download AutoDock Tools**.
   The AutoDock Tools download instructions appear in a Web browser.
   b. Download and install AutoDock to your local hard drive.
   c. In the AutoDock dialog box, click **Set AutoDockTools Directory** to select the path to where you installed the AutoDock Tools.

Working with the AutoDock Interface

The AutoDock Interface in Chem3D helps you perform the docking calculation. Preparing an AutoDock calculation involves several steps, each of which have been abstracted into a tab-based dialog in the AutoDock Interface. Following are the different steps involved in the docking calculation:

1. **Preparing receptor**. In this step, you define the receptor. The receptor may be either in a file or a model that is already open in ChemBio3D.
2. **Preparing ligand**. In this step, you define one or more ligand to dock to the receptor. The ligands may be either in a file or a model that is open in ChemBio3D.
3. **Defining groups**. In this step, named groups of atoms may be defined that are used in a post-docking analysis. Poses are analyzed to see if they do, or do not, interact with the named groups. These groups are especially useful to quickly determine if a pose makes a key interaction with the receptor. This is an optional step.
4. **Preparing GPF**. In this step, you prepare the Grid Parameter File (GPF). GPF is used to specify the files and parameters used in the calculation. Specifically, the docking cavity's location and size are defined in this step.
5. **Preparing DPF**. In this step, you prepare the Docking Parameter File (DPF). DPF is used to specify the files and parameters used for the docking calculation. Specifically, the parameters of the genetic search algorithm are defined in this step.
6. **Docking**. In this step, you perform the docking calculation.

After you perform the docking calculation, you can view the docking results using the **AutoDock Results** option under **Calculations > AutoDock Interface**.

Step 1: Preparing the receptor

You first load the receptor. The receptor may be either in a file or a model that is already open in ChemBio3D. Afterward, you use AutoDock to determine the charges and atom types throughout the molecule.

Note: *AutoDock accepts only molecules that it perceives as macromolecules. These are generally proteins or polypeptide sequences that consist of standard residues.*

To prepare the receptor:

1. Go to **Calculations**>**AutoDock Interface**>**Setup AutoDock Calculation**. The AutoDock Interface dialog box opens.

Tip: *While using AutoDock, you may want to ensure that the AutoDock Interface dialog box is always visible. To ensure that dialog box stays visible, right-click the dialog box title bar and select* ***Always on Top****.*

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2. Select the Prepare Receptor tab.
3. To load a receptor, do one of the following:
   - Click **Browse** to load a receptor into AutoDock from a file.
   - Click **Import** to load a receptor that is currently open as a model in ChemBio3D.

Note: *The model must be in the active ChemBio3D window before you can import it.*

4. (Optional) To prevent AutoDock from assigning new charges to the receptor, select **Preserve all input charges**.
5. To compute the receptor charges and determine atom types, click **Run**.

After determining the charges and atom types, AutoDock saves the results in the AutoDock work folder.

Note: *The file is saved in the AutoDock work folder in .pdbqt file format, and the default file name will be of the format <InputFileName>_adv.pdbqt. For example, if "receptor.pdb" is the input file that you have imported, then the default file name of the output file is "receptor_adv.pdbqt".*

A report of the results and any errors that may have occurred appear at the bottom of the AutoDock Interface dialog box.
To set the AutoDock work folder, go to the General tab and click **Browse Work Folder**.

- To clear the window, click **Clear Log**.
- To save the log to file, click **Save Log**. A log file is saved in the working directory.
- To change the folder in which the files are saved or to open the log file, click **Browse Work Folder**.

Caution: *Do not close the AutoDock Interface after you prepare the receptor. If you close the dialog box before completing the docking calculation, you will need to start over.*

Step 2: Preparing the ligand

After preparing the receptor, you must prepare one or more ligands to dock to it. The ligand may be either in a file or a model that is open in ChemBio3D. You then use AutoDock to determine the rotatable bonds and atom types in the ligand. AutoDock uses this data to describe the conformational space and interaction types of the ligand.
To prepare the ligand:

1. In the AutoDock Interface dialog box, select the Prepare Ligand tab.
2. To load a ligand, do one of the following:
   - Click **Browse** to load a ligand into AutoDock from a file.
   - Click **Import** to load a ligand that is currently open as a model in Chem3D.

   Note: *To import a model, the model must be in the active ChemBio3D window.*
3. (Optional) Browse to or import other ligands as desired. The ligands you load are listed under **List Ligands**.
4. To determine the rotatable bonds in the ligand and its atom types, click **Run**.

After determining the rotatable bonds and atom types, AutoDock saves the results in the AutoDock work folder.

Note: *The file is saved in the AutoDock work folder in .pdbqt file format, and the default file name will be of the format <InputFileName>.pdbqt. For example, if "ligand.mol2" is the input file that you have imported, then the default file name of the output file is "ligand.pdbqt".*

A report of the results and any errors that may have occurred appear at the bottom of the AutoDock Interface dialog box.

- To clear the window, click **Clear Log**.

- To save the log to file, click **Save Log**.
- To change the folder in which the files are saved, click **Browse Work Folder**.

Step 3: (Optional) Defining groups

An atom *group* represents a binding site of interest that you define in the receptor cavity. A group includes all atoms (up to 10) you choose for the binding site and a radius (in Angstroms) that you define around the binding site.

Note: *You do not have to define atom groups to perform docking calculations. However, if you do, you must prepare the receptor before you can define groups for it. See* *"Step 1: Preparing the receptor" on page 157*

When you perform docking, AutoDock examines each ligand pose. Afterward, ChemBio3D determines whether any of the ligand atoms are within the radius of each group you define. When you define a group, you assign it as either an *exclusion zone* or an *inclusion zone*. An exclusion zone is a binding site in which all ligand atoms in the pose must be positioned outside the group radius. An inclusion zone is a binding site in which at least one ligand atom in the pose must be positioned inside the group radius.

Each named group generates a new column in the final docking table in Chem3D with the name of the named group as the column heading. This table has one row per pose. A value of "true" is displayed if the pose obeys the inclusion or exclusion rule defined with the named group.

To define a group:

1. In the receptor model, select up to 10 atoms to designate as a named group for the ligand.
2. In the AutoDock Interface, select the Define Groups tab.
3. Click **Add New Group From Selected Atoms**. Each new group you create appears in a list in the dialog box.
4. In the list in the dialog box, enter a **Group Name** for the group.
5. Enter a binding **Radius** for the group. The default is 3.5 Angstroms.This is implemented by placing a sphere of the given radius around each atom in the named group.
6. Select whether AutoDock should consider the group as either an **Exclusion Zone** or an **Inclusion Zone**.
7. (Optional) Repeat the steps above to define more groups.

After you define your groups, you use them to prepare the cavity for docking.

Step 4: Preparing the cavity (prepare GPF)

The cavity is the empty space inside the receptor into which the small molecules will bind. It is necessary to define the cavity to direct AutoDock where to explore the docking space. To define a cavity, you select atoms or groups at points of your choosing along the cavity boundary. ChemBio3D calculates the centroid of the cavity using your selection(s) and defines a grid box around the centroid. You adjust position and size (number of grid points and spacing between points) of the grid box to enclose the selected atoms or groups along the cavity boundary that you want AutoDock to use in the calculation. The AutoDock calculation is confined to the defined grid box. If any named groups have been defined in Step 3, make sure that these groups are excluded inside the grid box; otherwise the ligand will have no chance to interact.

Before computing the docking, AutoDock builds a series of grid maps, one per ligand atom type. Each grid map is constructed by placing a probe atom of an atom type at each grid point and computing its interaction energy with the receptor. During docking, a ligand is posed inside the grid box and its interaction energy with the protein is computed using the grid maps.

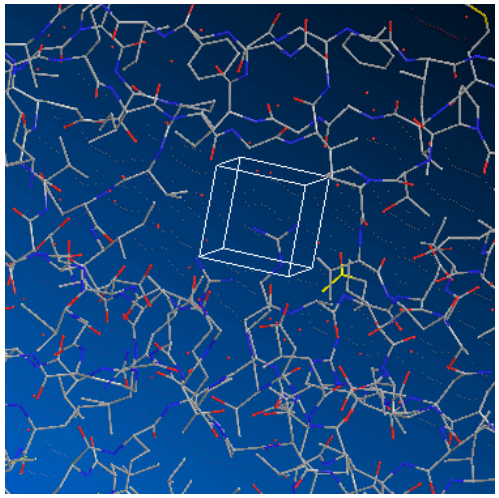

Figure 8.1: A protein with the grid box inside a cavity (the box is shown here in white for clarity).

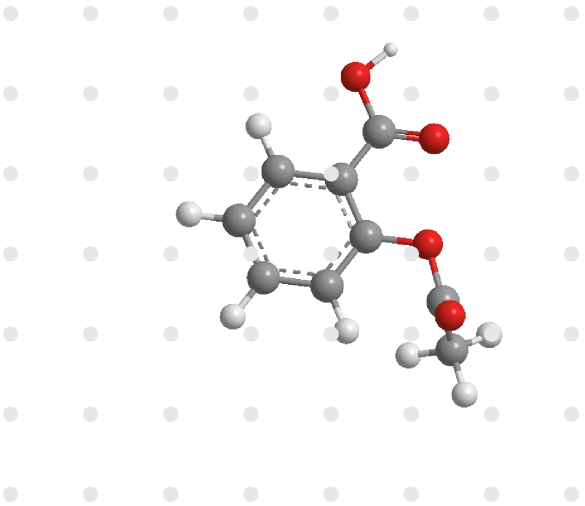

Figure 8.2: An illustration of the grid box in two dimensions with a ligand pose and calculated energy grid points.

To prepare the cavity:

1. In the AutoDock Interface, select the Prepare GPF tab.
2. In the model window, select at least one atom or group on the cavity boundary within the receptor.

***Tip:** Consider selecting at least three atoms or groups in different locations along the boundary for a more accurate cavity calculation.*

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3. Click **Centroid of the Selection**. AutoDock calculates the centroid of the cavity based on your selection(s). This is a convenient tool to set the initial location of the grid box. Alternatively you can click "Set GridBox to Receptor Size" to place a box around the whole structure.
4. (Optional) To display the grid box in the model window, select **Display Grid Box**. The center of the grid box is positioned at the center of the cavity.You can also choose a color for the grid from the drop-down box.
5. Under Centroid of the Grid Map, enter **X**, **Y**, and **Z** coordinates to move the grid box as necessary.
6. Under Number of Grid Points, enter the number of grid points to use in the **X**-, **Y**-, and **Z**-axes. The grid box resizes as you edit the values.

   Note: *To change any of the X, Y, or Z values, either enter a value in the text box or use the scroll arrows.*

7. Select the **Spacing of Grids** in Angstroms. This grid box resizes after you enter a value.
8. (Optional) To edit the GPF file manually, click **Edit** under Advanced Options. The GPF file opens in a text editor and you can make necessary changes.

Caution: *It is not advisable to edit the GPF file manually. Any mistake in the manual editing may block AutoDock from performing the docking job correctly.*

9. Click **Run**.

AutoDock saves the results in the AutoDock work folder. A report of the results and any errors that may have occurred appear at the bottom of the AutoDock Interface dialog box.

- To clear the window, click **Clear Log**.
- To save the log to file, click **Save Log**.
- To change the folder in which the files are saved, click **Browse Work Folder**.

Step 5: Selecting pose parameters (Prepare DPF)

During the docking calculation, AutoDock determines each possible pose the ligand can undergo and chooses the best poses to use.

The pose parameters you enter determine how AutoDock will use the poses to calculate the docking:

No. of Individuals in Population. This is the number of individuals in the population. Each individual is a coupling of a genotype and its associated phenotype.The number must be a positive integer. Typical values that are often used range from 50 to 150.

Generations. The number of times a new "breed" of molecules is created (using Generic Algorithm rules) from the previous generation. Larger molecules will need more generations. The number must be a positive integer. The default value is 27000. Typical values that are often used range from 5000 to 30000. Run time for each molecule increases linearly with this number.

Energy Evaluations. Upper limit on the total number of energy evaluations performed in a single GA run over all generations. A sort of "safety valve" to stop the calculation running forever. The number must be a positive integer. The default value is 250000.

Docking. Number of automated docking runs. Typical values that are often used range from 5 to 15. Docking calculation time increases as this value increases.

To enter the pose parameters:

1. In the AutoDock Interface, select the Prepare DPF tab.
2. Enter the pose parameters in the **Parameter** fields. AutoDock saves the values in the dpf file displayed in the Advanced Options field.
3. (Optional) To edit the DPF file manually, click **Edit** under Advanced Options. The DPF file opens in a text editor and you can make necessary changes.

Caution: *It is not advisable to edit the DPF file manually. Any mistake in the manual editing may block AutoDock from performing the docking job correctly.*

4. Click **Run**.
5. For an in-depth explanation on these values, see the AutoDock Web site.

Step 6: Docking

By the time you are ready to start the docking calculation, AutoDock has stored in log files all needed information about the ligand, receptor, and the binding sites. You can edit this information in the log files before you run the calculation.

AutoDock uses two files namely, Grid Parameter File (GPF) and Docking Parameter File (DPF) to record information about the ligand, receptor, and the binding sites.

GPF specifies the files and parameters used in the calculation such as the size and location of the grid, the atom types that will be used, and other parameters for calculation of the grids. The grid parameter file usually has the extension ".gpf".

DPF specifies the files and parameters used for the docking calculation. It also includes the map files that will be used for the docking, the ligand coordinate files, and parameters for the search. The docking parameter file usually has the extension ".dpf".

Caution: *Only expert users should edit the AutoDock log files. Otherwise, the AutoDock calculation may produce unwanted results.*

1. In the AutoDock Interface, select the Docking tab.
2. (Optional) Click **Edit GPF** to edit the cavity parameters log file.
3. (Optional) Click **Edit DPF** to edit the pose parameters log file.
4. Click **Run AutoDock**.

After AutoDock calculates the docking, AutoDock reports that the docking job is complete and asks whether you want to display the results.Results dialog box appears. You can review the results in the ChemBio3D structure Browser.

Note: *The result is saved in the AutoDock work folder in .dlg file format, and the default file name will be of the format <ligand file name>_<receptor file name>_adv.dlg. For example, if "receptor.pdb" is the receptor name, and ligand.mol2 is the ligand name, then the default file name of the output file is "ligand_receptor_adv.dlg".*

Step 7: Viewing Docking Results

To view the docking results, follow the steps mentioned below:

1. Go to **Calculations >AutoDock Interface>AutoDock Results**.
2. In the AutoDock Results dialog box, click **Prepare Results**. You will be asked to open the docking log file.
3. Open the docking log file. The file opens in ChemBio3D.

The results appear as a model in the ChemBio3D Model window. The file includes the receptor and all poses that meet the parameters you set for the docking.
To view previous results:

1. In the AutoDock Results dialog box, click **Browse Results** under Previous Results.
2. Browse to the location where you have saved the docking log file.
3. Open the log file. The file opens in ChemBio3D.

To examine the poses:
The docking results are displayed in the structure browser, and the named group and various docking energy levels are displayed in various columns in the structure browser.

1. In the model window, ensure that the docking results model is the active tab.
2. Go to **View**>**Structure browser**. All poses in the file are listed.
3. In the structure browser, select/deselect checkboxes to display/hide poses in the model window.

References

See these references for more information on AutoDock.

- The AutoDock User Guide
- General AutoDock FAQ
- AutoDock parameter suggestions
- Docking and energy evaluation suggestions
- Ligand limitations

Tutorials

This section provides examples of some basic tasks you can perform with ChemBio3D 13.0.

Building models

- "Tutorial 1: Building Models in 2D" on page 164
- "Tutorial 2: Building with bond tools" on page 165
- "Tutorial 3: Building models with Text" on page 172

Examining models

- "Tutorial 4: Examining Conformations" on page 176
- "Tutorial 5: The Dihedral Driver " on page 179
- "Tutorial 6: Overlaying Models" on page 181
- "Tutorial 7: Aligning Models" on page 183
- "Tutorial 8: Viewing Orbitals" on page 186
- "Tutorial 9: Mapping Surfaces " on page 187
- "Tutorial 10: Partial Charges" on page 190

Using calculation engines

- "Tutorial 11: Rotamer Analysis" on page 192
- "Tutorial 12: Calculating Rotational Bonds" on page 195

Before starting the tutorials, we recommend that you choose the default settings and an appropriate display so that your results are similar to what you see in this guide.
To apply the default settings:

1. Go to **File**>**Model Settings**.
2. In the Model Settings dialog box, click **Reset to Default**.
3. Click **OK**.

To view models as they appear in these tutorials:

1. Go to **View**>**Toolbars**>**Model Display**.
2. On the **Model Display** toolbar, select the **Display Mode** drop-down menu and choose **Cylindrical Bonds**.

Building models

Tutorial 1: Building Models in 2D

In this tutorial, you build a model of phenol using the ChemDraw panel. When you draw in the ChemDraw panel your two-dimensional ChemBioDraw structure appears as a ChemBio3D model.

1. Go to **File**>**New** to open a new model window.
2. Go to **View**>**ChemDraw Panel.**The ChemDraw panel opens.

Tip: *The ChemDraw panel is docked and hidden by default. To keep the panel open when it is docked, click the pin on the upper right.*

3. In the top left corner of the panel, select **LiveLink** ( ).
4. Click in the ChemDraw panel. The ChemDraw tools palette appears.
5. On the ChemDraw tools palette, select the Benzene tool.
6. Click in the ChemDraw panel to draw a benzene ring. The ChemDraw structure is converted to a 3D representation.

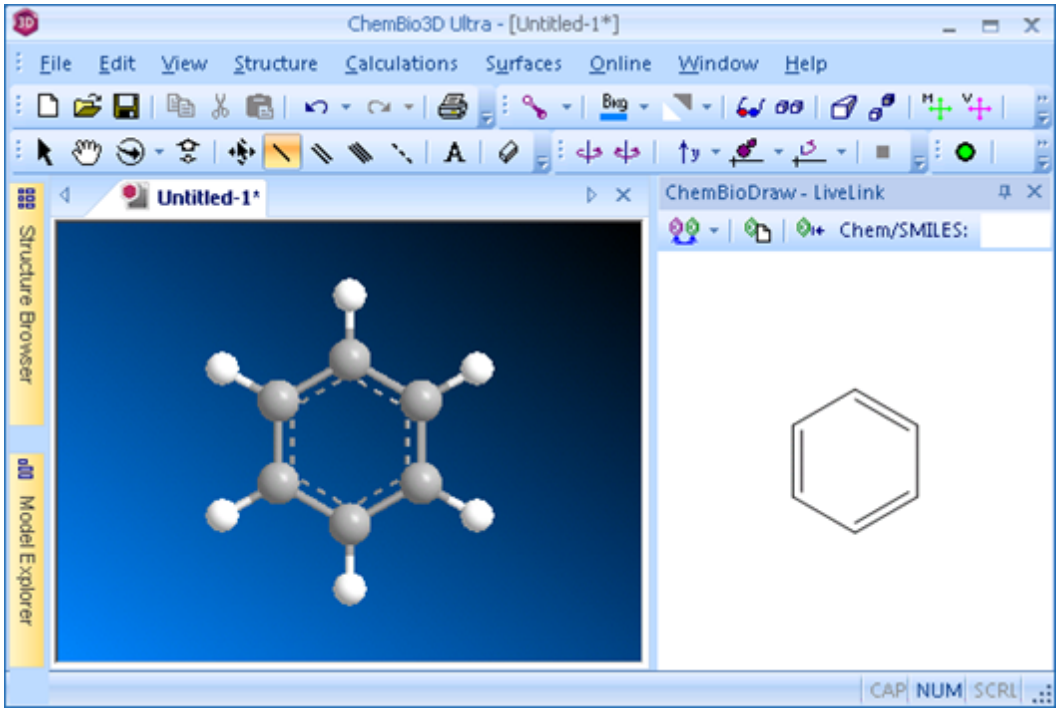


Figure 9.1: A 3D model of benzene.

To change the benzene ring to phenol:

1. Select a bond tool in the Building toolbar.
2. Double-click any hydrogen in the 3D model. A text box appears.
3. Type OH (use capital letters) in the text box and press ENTER.

The phenol molecule appears in the Model window and in the ChemDraw panel.

Tutorial 2: Building with bond tools

In this tutorial, we use a model of ethane to demonstrate some fundamental ChemBio3D 13.0 features. We show how to rotate models, view bond properties, and add atom serial numbers. First, we build the ethane model:

1. Click the Single Bond tool in the Building toolbar.
2. Click-drag in the Model window and release the mouse button.

A model of ethane appears since you have draw a single bond with default carbon atoms and default H placement.

Rotating models

To see the three-dimensional features of your model, rotate it using the Rotate tool. You have a choice of rotating free-hand; around the X, Y, or Z axis; or around a selected bond. The status bar displays the angle of rotation.

To perform free-hand rotation:

1. Select the Rotate tool in the Building toolbar.
2. Click-drag near the center of the model window.

Note: *The axis of rotation is determined by the direction of the drag; the axis of rotation is orthogonal to the drag axis in the plane of the screen. The Rotate tool rotates the view only; it does not change atoms' Cartesian coordinates.*

To rotate around an axis:

1. With the Rotate tool selected, move the cursor to the top edge of the model window. The rotation bars appear.
2. Click-drag the rotation bar at the top of the model window. The model rotates around the Z-axis.
3. (Optional) Click-drag the right and bottom rotation bars to rotate the model around the X- and Y-axes.

Note: *Rotation bars appear only when you use the Rotate tool.*

To rotate around a bond:

1. Click the Select tool in the Building toolbar.
2. Select a bond in your model.
3. Select the Rotate tool.
4. Click-drag the **Rotate About Bond** rotation bar on the left side of the Model window.

Bond and atom properties

Many model properties are available at a glance. Hover the cursor over any bond or atom to view its properties.

Note: *To choose the properties that appear, go to* ***File>Preferences****. In the Popup Info. tab, select the popup information you want shown.*

To see bond and atom properties of ethane.

1. Click the Select tool in the Building toolbar.
2. Move the cursor over a carbon atom. An information box appears next to the atom.

By default, the first line contains the atom label, either C(1) or C(2). The second line shows the name of the atom type, C Alkane. Other information may appear depending on your selected preferences.

Note: *To view the information dialog box, the following options must be selected under* ***File > Preferences > Popup Info***

- Atom Type
- Measurement
- Bond Length

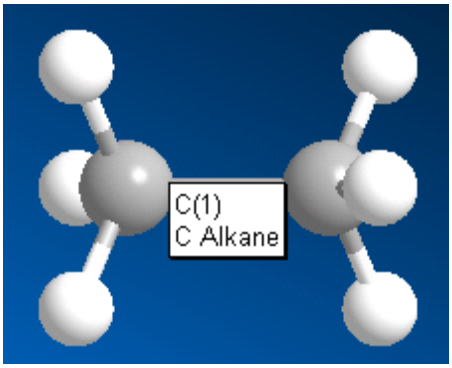


Figure 9.2: Viewing the atom label.

3. Move the pointer over the C-C bond to display its properties.

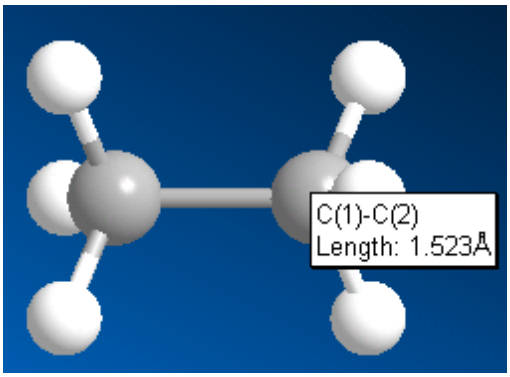


Figure 9.3: Viewing bond length.

To display bond angles, select three atoms that are adjacent to each other.

1. SHIFT+click **C(1)**, **C(2),** and **H(7)**.
2. Point to any of the selected atoms or their connecting bonds.

The angle for the selection appears.

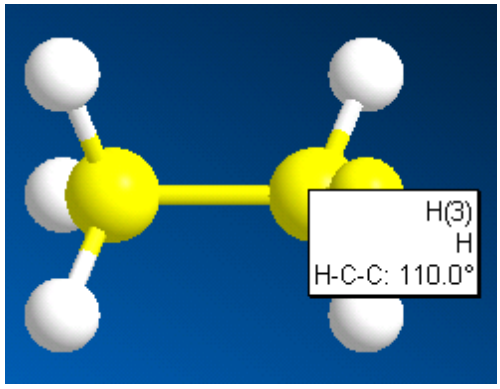


Figure 9.4: Viewing bond angles.

To display the dihedral angle of adjacent atoms:

1. SHIFT+click both carbons and one hydrogen on each carbon. The atoms form a dihedral angle.
2. Point to any portion of the selection. The dihedral angle measurement appears.

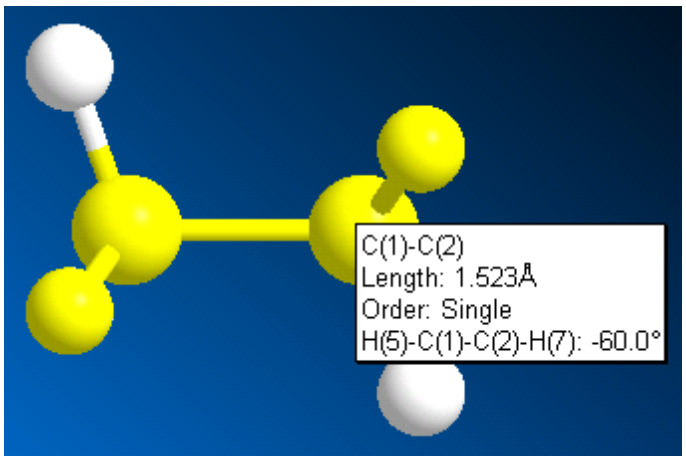


Figure 9.5: Viewing a dihedral angle.

You can also change the bond order. In this case, we can change the ethane model to ethylene:

1. Click the Double Bond tool in the Building toolbar.
2. Drag the mouse from C(1) to C(2).
3. Point to the C(1)-C(2) bond. Notice that the bond length has decreased and the bond order has increased.

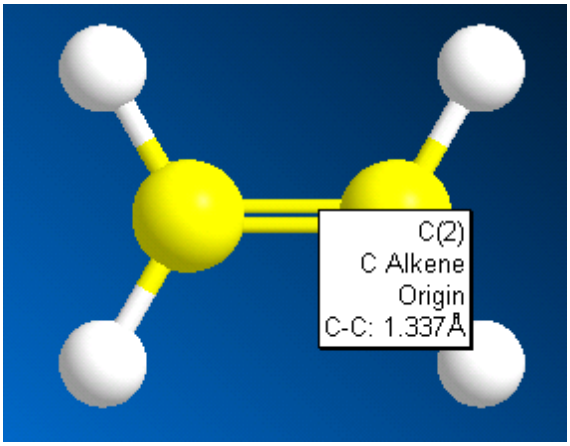


Figure 9.6: Model of ethylene.

Building Cyclic Compounds

You can continue building on the ethylene model to create cyclohexane.

First, change ethylene back to ethane:

1. Click the Select tool in the Building toolbar.
2. Right-click the double bond.
3. In the context menu, go to **Set Bond Order**>**Single**.

Hiding Hydrogens

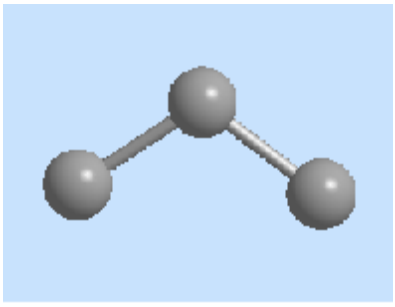
Sometimes, you may want to hide the hydrogen atoms in your model to make building easier. The hydrogens are still there and chemically active; they are just not in view.

To hide the hydrogens, go to **View**>**Model Display**>**Show Hydrogen Atoms**>**Hide**.

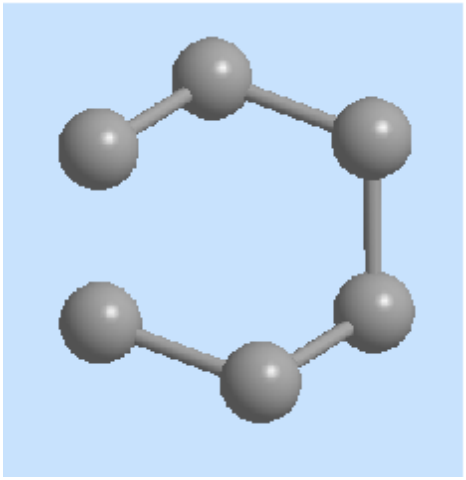
Adding atoms

Here we add more atoms to the model to create a cyclohexane ring:

1. Click the Single Bond tool in the Building toolbar.
2. Drag downward from the left carbon. Another C-C bond appears.

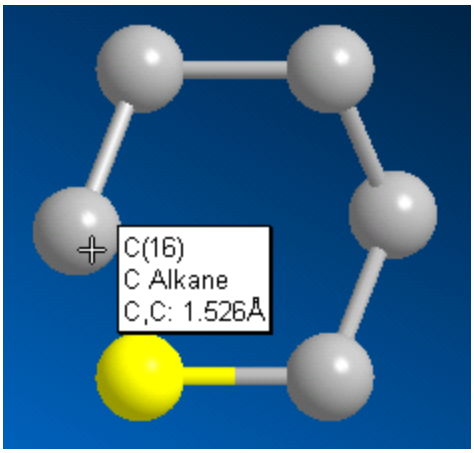


3. Continue adding bonds until you have six carbons as shown below.



Create a ring

1. Drag from one terminal carbon across to the other.



2. Release the mouse button to close the ring.

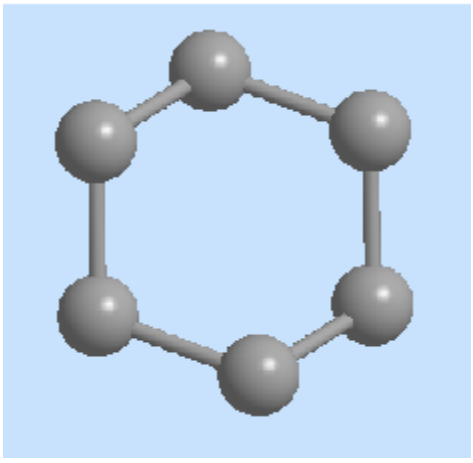


Figure 9.7: Building cyclohexane with the bond tool.

Serial Numbers and Labels

Whenever you build or examine a model, atoms of the same type all look the same (as they should). However, it is sometimes convenient to distinguish one from another. This is where atom serial numbers and labels become useful.

1. Go to **View**>**Model Display**>**Show Serial Numbers** or click the Serial Number icon on the Model Display toolbar.
2. Go to **View**>**Model Display**>**Show Atom Symbols,** or click the Atom Symbol icon on the Model Display toolbar.

Note: *The serial numbers that appear do not reflect a normal ordering because you started with a smaller model and built up from it.*

If you want, you can change the numbering order by choosing which atom is numbered first.
To renumber the atoms:

1. Select the Build from Text tool .
2. Click the first atom you want to number. A text box appears on the atom.

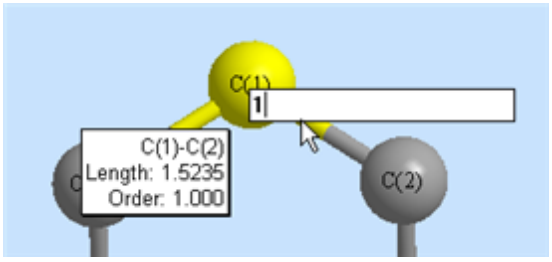


Figure 9.8: Adding atom symbols and numbers.

3. Type the number you want to assign to this atom (1 for this example).
4. Press ENTER . The first atom is renumbered as (1).
5. Double-click each of the atoms in the order you want them to be numbered.

6. Go to **View**>**Model Display**>**Show Hydrogen atoms**>**Show All** and examine the model using the Rotate Tool.

Structure Cleanup

As you build a model, you may accidentally distort bond angles and bond lengths. To correct for this:

1. Go to **Edit**>**Select All**. All the atoms in the model are selected.
2. Go to **Structure**>**Clean Up**.

Saving the model

Before moving to the next tutorial, you may want to save and close your model.

1. Go to **File**>**Save**.
2. Select a directory in which to save the file.
3. Type tut2 in the text box at the bottom of the dialog box.
4. Click **Save**.
5. Click the model window to activate it.
6. Go to **File**>**Close Window**.

Tutorial 3: Building models with Text

This tutorial illustrates alternative methods for building models using the Build from Text tool.

Build From Name

Using the Build from Text tool you can build a model by specifying its compound name. To build the model:

1. Select the Build from Text tool in the Building toolbar.
2. Click anywhere in the model area.
3. Enter the compound name (for example `cyclohexane`) in the text box that appears.
4. Press ENTER. The model appears in the model window.

Replacing Atoms

Using the cyclohexane model, change a hydrogen atom into a carbon atom:

1. Click Build from Text tool.
2. Click any hydrogen atom. A text box appears.
3. Type uppercase “C” and press ENTER. The hydrogen changes to a carbon.

Note: *Element symbols and substructure names are case sensitive. You must type an uppercase C to create a carbon atom.*

If rectification is turned on, the carbon valence is saturated with hydrogens. See "Rectifying atoms" on page 27.

You don’t have to select the Text tool to use it. Double-clicking with the Move Objects tool has the same effect as single-clicking with the Text tool. For example, replace two more hydrogens using this method:

1. Select the Rotate tool so that you can rotate your model to get a better view of what you are building.
2. Double-click two more hydrogens with the Move Objects tool to change them to methyl groups.

Tip: The "C" you entered previously in the Text tool remains as the default until you change it. You only have to double-click with the Build from Text tool.

Saving the File

To save the file:

1. Go to **File**>**Save As**.
2. Type tut3a.
3. Select a directory in which to save the file and click **Save**.

Save a copy of the model using the name tut3b.

These two copies of your model will be used in later tutorials.

Using Labels to Create Models

You can also create models by typing atom labels (element symbols and numbers) in a text box.

For example, to build 4-methyl-2-pentanol shown below:

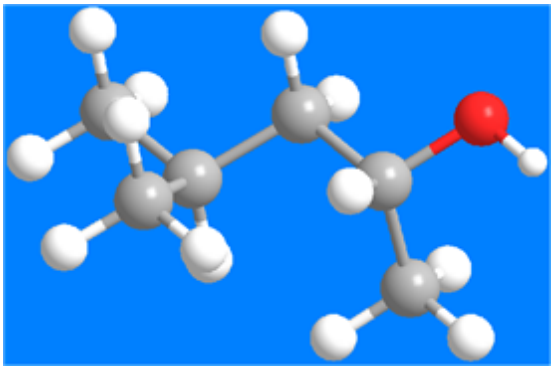


Figure 9.9: Creating a model with the text box.

1. Go to **File**>**New** or click the New tool on the Standard toolbar.
2. Click the Build from Text tool .
3. Click in the model window. A text box appears.
4. In the text box, type either `CH3CH(CH3)CH2CH(OH)CH3` or `4-methyl-2-pentanol`.

You type labels as if you were naming the structure: pick the longest chain of carbons as the backbone, and specify other groups as substituents. Enclose substituents in parentheses after the atom to which they are attached.

5. Press ENTER.

Tip: The Text building tool also accepts structures in SMILES notation, either typed in or cut and pasted from other documents.

Name=Struct

Another way to build this model is to use Name=Struct.

To create the model using Name=Struct:

1. Right-click an empty space in the ChemDraw panel and select **Structure**>**Convert Name to Structure** in the context menu.
2. In the Insert Structure dialog box, type **`4-methyl-2-pentanol`** and click **OK**. The structure appears in the ChemDraw panel.
3. So that model appears in the Model window, ensure that LiveLink is selected at the top of the ChemDraw panel.

Tip: *To temporarily activate the Select tool, hold down the letter S on your keyboard while working with any building tool.*

Stereochemistry

You cannot specify stereochemistry when you build models with labels. For example, 1,2-dimethyl cyclopentane appears in the *trans* conformation by default. However, you can modify the default structure to show the *cis*-isomer.

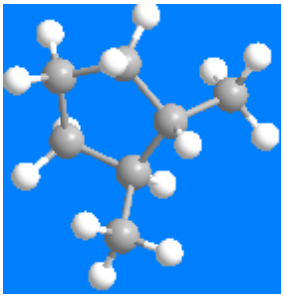


Figure 9.10: More complex models with the text box.

To illustrate, first, build the default structure:

1. Go to **File**>**New**.
2. Click Build from Text tool .
3. Click in the empty space in the model window.
4. Type 1,2-dimethyl cyclopentane.
5. Press ENTER . The *trans*-isomer appears.
6. Go to **Edit**>**Select All**.
7. Go to **Structure**>**Clean Up**.

Now invert it to display the *cis*-isomer:

1. Click the Select tool .
2. Select **C(1)**.
3. Go to **Structure**>**Invert**.

The *cis*-isomer appears. You can rotate the model to see the differences between the isomers after you invert the molecule.

Using Substructures

Labels are useful for building simple structures. However, to make larger, more complex structures, you may find it easier to use a combination of labels and predefined substructures.

Over 200 substructures are predefined in ChemBio3D 13.0. These include the most commonly used organic structures.

Tip: *Predefined substructures are listed in the substructures.xml file. To view the list, go to* ***View>Parameter Tables>Substructures****. Text you type in the text box is case sensitive (you must type it exactly as it appears in the Substructures table).*

To build a model of nitrobenzene using substructures:

1. Go to **File>New**.
2. Click Build from Text tool .
3. Click the empty space in the Model window.
4. Type Ph(NO2) in the text box.
5. Press ENTER. A model of nitrobenzene appears.

The substructure in this example is the phenyl group, as indicated by “Ph”. Substructures are defined with specific attachment points for other substituents. For phenyl, the attachment point is C(1).

To build a peptide model:

1. Go to **File>New**.
2. Click Build from Text tool .
3. Click an empty space in the Model window. A text box appears.
4. Type H(Ala)12OH and press ENTER .
5. Rotate this structure to see the alpha helix that forms.

Changing model display

To change the model display type:

1. Click the arrow on the right side of the Model Display Mode tool on the Model Display toolbar.
2. Select **Wire Frame** as the Model Type.

Tip: *You can also click the Display Mode icon. Successive clicks cycle through the Display Mode options.*

---

3. Select the Rotate tool , and rotate the model so you are viewing it down the center of the helix.
4. Use the Model Display Mode tool to choose **Ribbons** as the model type to see an alternative display commonly used for proteins.

Examining models

Tutorial 4: Examining Conformations

This tutorial uses steric energy values to compare the eclipsed and staggered conformations of ethane. You first create the staggered conformation and calculate the steric energy. You then do the same for the eclipsed conformation. Afterwards, you compare the two steric energy values.

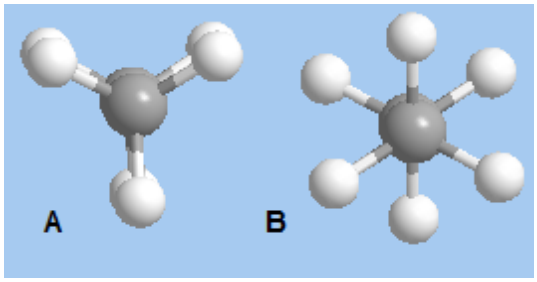


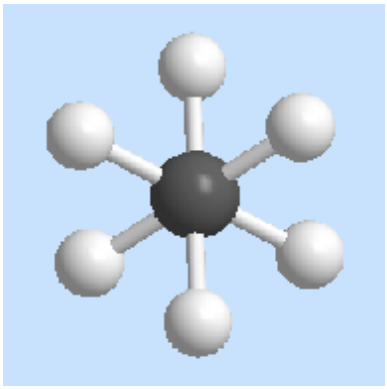
Figure 9.11: The steric energies of the eclipsed (A) and staggered (B) conformations of ethane are calculated in this tutorial.

To create the staggered conformation:

1. Using the Single Bond tool , draw a model of ethane in the model window.

1. Select the Rotate tool on the Building toolbar.
2. Click and drag to rotate the model.
3. Stop dragging when you have an end-on view of ethane.

This staggered conformation, where the hydrogen atoms on adjoining carbons are a maximum distance from one another, represents the most stable conformation of ethane. The global minimum in the potential energy plot represents this conformation.



To calculate the steric energy of this conformation:

1. Go to **Calculations**>**MM2**>**Compute Properties**. The **Compute Properties** dialog box appears.
2. In the Properties tab, select **Pi Bond Orders** and **Steric Energy Summary**.

Tip: *Use SHIFT+click to select the properties.*

---

3. Click **Run**.

The Output box appears beneath the model window, with steric energy results displayed. The last line displays the total energy.

```
Output
MM2 Calculation completed successfully
------------MM2 Properties------------
Note: All parameters used are finalized (Quality = 4).
  Stretch:                0.0000
  Bend:                   0.0005
  Stretch-Bend:           0.0000
  Torsion:                0.0000
  Non-1,4 VDW:            0.0000
  1,4 VDW:                0.9761
Total Energy:             0.9766 kcal/mol

The total energy for this frame:     0.977 kcal/mol
Calculation ended
-----------------------------------------
```

Note: *The values of the energy terms can vary depending on your computer processor.*

To obtain the eclipsed conformation of ethane, you rotate a dihedral angle (torsional angle). This is a common way to analyze the conformational space for a model.
To view dihedral angles:

1. Go to **Structure**>**Measurements**>**Generate All Dihedral Angles**.

   All of the model's dihedral angle measurements are added to the Measurement table. To help keep visual track of the atoms as you change the dihedral angle you can display the serial numbers and element symbols for the selected atoms.
2. In the Measurement table, select the **Display** check box for one of the listed dihedral angles, such as H(3)-C(1)-C(2)-H(8).

   Note: *To view in the model which atoms you are selecting in the Measurements window, go to* ***View***>***Model Display*** *and select* ***Show Serial Numbers*** *and* ***Show Atom Symbols****.*
3. Click the arrow next to the Rotate tool , and tear off the rotation dial by dragging on the blue bar at the top.
4. At the bottom of the Rotation Dial, select either dihedral rotation button.
5. Do one of the following:

   a. Enter the value 0.0 in the degrees display box.
   b. Click and drag the green button on the rotation dial to 0.0.

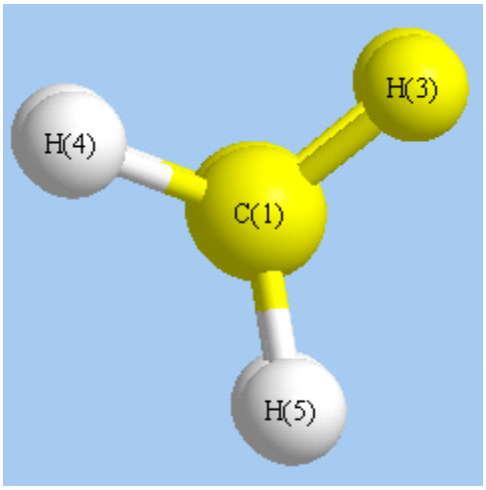


Figure 9.12: Rotating a dihedral angle.

To compute steric energy:

1. Go to **Calculations**>**MM2**>**Compute Properties.**

Note: *The property tab defaults should remain as in the previous calculation.*

2. Click **Run**.

The final line in the Output box appears.

Output

```
MM2 Calculation completed successfully
------------MM2 Properties------------
Note: All parameters used are finalized (Quality = 4).
  Stretch:                  0.0000
  Bend:                     0.0005
  Stretch-Bend:             0.0000
  Torsion:                  2.1330
  Non-1,4 VDW:              0.0000
  1,4 VDW:                  1.7726
Total Energy:               3.9061 kcal/mol

The total energy for this frame:     3.906 kcal/mol
Calculation ended
-----------------------------------------
```

Figure 9.13: The Output box.

Note: *The values of the energy terms can vary slightly based on the type of computer processor you are using.*

The steric energy for the eclipsed conformation (~3.9 kcal/mole) is greater in energy than that of the staggered conformation (~1 kcal/mole), indicating that the staggered configuration is the conformation that is more likely to exist.

Tutorial 5: The Dihedral Driver

The dihedral driver graphs the conformational energy of a model by varying up to two dihedral angles that you select. At each dihedral angle value, the model energy is minimized using the MM2 force field and the steric energy of the model is calculated and graphed. After the calculation is complete, you can view the data to locate the conformations with the lowest steric energy values and use these as starting points for further refinement in locating a stationary point.

In this tutorial, we demonstrate a single angle plot using the dihedral driver on ethane.

1. Build a model of ethane.
2. Select the carbon-carbon bond.
3. Go to **Calculations**>**Dihedral Driver**>**Single Angle Plot.**

The Dihedral Driver Chart opens. When the calculation is complete, a graph displays the energy versus the angle of rotation around the selected bond.

To view the conformation:

1. In the chart, click any point along the curve. The dihedral bond in the model rotates the angle you select in the graph.
2. To see the conformation energy through a range of rotation angles, click and drag across the chart while viewing the model.

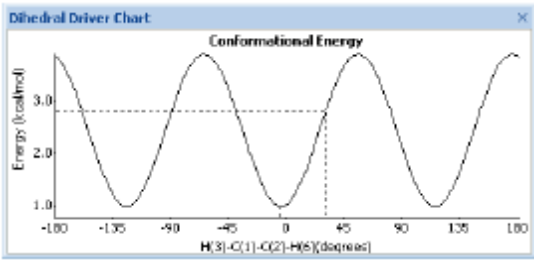


Figure 9.14: A dihedral driver single-plot chart for ethane.

Note: *The dihedral rotates in 5° increments through 360° for a total of 72 conformations to produce the graph. You can view the minimized energy values for each point in the Output window.*

To rotate the other dihedral angle (other end of the bond), right-click in the Dihedral Driver Chart and choose **Rotate other End**.

Recomputing with minimization

Simple rotation does not take into account other conformational changes that may occur upon dihdral rotation (e.g. angle bending). As a result, your model may depict high-energy strain at various bonds or conformational strain between atoms. As a result, your model may not accurately represent the actual molecule, and correspondingly the graph in the **Dihedral Driver Chart** dialog box may not be accurate. To obtain an accurate graph, consider recomputing with energy minimization.

To produce the graph with energy minimization[1], right-click on the **Dihedral Driver Chart** dialog box and select **Recompute with Minimization**.

Rotating two dihedrals

To rotate two dihedrals:

1. SHIFT+click two adjacent bonds to select them.
   In this case, the middle atom's position remains fixed.
2. Go to **Calculations>Dihedral Driver>Double Angle Plot**.

The Output window opens. When the calculation is completed, a graph displays theta 1 vs. theta 2.

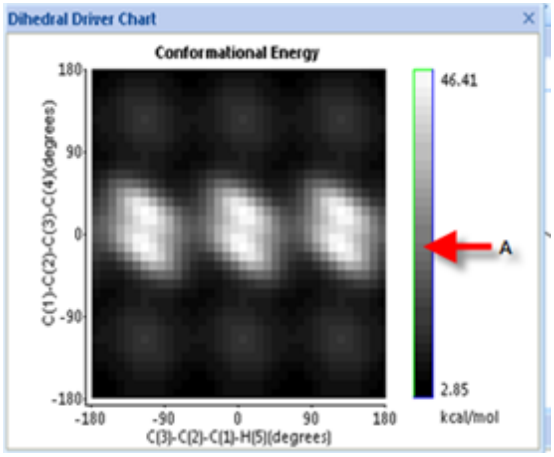


Figure 9.15: The dihedral driver Chart; A: Legend bar.

Note: *The chart is the result of rotating one angle through 360° in 10° increments while holding the other constant. The second angle is then advanced 10° and the operation is repeated.*

To view the conformation/energy at any point, click the point in the chart. The model display rotates both dihedrals to the selected conformation/energy.

Customizing the dihedral chart

You can change how the chart colors and how the chart displays data.

Setting legend graph scale

By default, the chart displays data on a linear scale. To change the scale from linear to logrithmic (applies only to double-dihedral charts):

1. Right click anywhere on the chart.
2. From the context menu, select **Set Legend Function**.
3. Select the desired log option. The color map changes accordingly.

[1] In computational chemistry, energy minimization methods are used to compute the equilibrium configuration of molecules and solids.

Exchanging axes

You can exchange the axes in a double angle dihedral chart. Right-click the chart and select **Exchange Axis**.

Recompute with minimization

If your model contains distorted bonds (typically, by moving atoms), you can minimize the energy and recompute the dihedral chart. Click the chart and select **Recompute with Minimization**.

Peak Truncation

In double dihedral charts, you can truncate the high energy values in bad conformations to focus on more meaningful conformation. To change the upper and lower bound of the legend, click+drag the top and bottom of the legend bar. This changes the color map. You can get the energy/conformation at any point on the color map by clicking that point. You can also focus on the local minima using peak truncation by dragging the upper bound and ignoring all conformations having higher energy than the upper bound value.

Setting graph colors

Right-click the chart to set the rotation interval used for the computation. Once reset, the dihedral computation is repeated with the new interval values. You can also select display colors for the chart, background, coordinates, and labels.

Setting graph resolution

By default, the conformational energy is calculated in 5° increments. To change the resolution, right-click the chart, select **Set Resolution**, and choose a new value from the list.

Copying, saving, and printing the chart

Right-click the chart and choose from these options:

- **Copy Picture** to copy the chart to the clipboard.
- **Copy Data** to copy the chart data to the clipboard.
- **Save Picture** to save the picture as an image file.
- **Print** to print the chart.

Tutorial 6: Overlaying Models

Use overlays to compare the structural similarities between two models or conformations of the same model. ChemBio3D 13.0 provides two overlay techniques. You can use either a *fast overlay* algorithm or a manual method based on minimization calculations.

This tutorial describes the fast overlay method. For the minimization method, see "Comparing models by overlay" on page 60. The minimization method is more accurate, but the fast overlay algorithm is more faster. In both tutorial examples, you superimpose a molecule of methamphetamine on a molecule of epinephrine (Adrenalin) to demonstrate their structural similarities.

To overlay the two molecules, you must first create them:

1. Go to **File**>**New.**
2. Go to **View**>**Model Explorer** (if the model explorer is not already open).

3. Choose the Build from Text tool from the Building toolbar and click in the model window. A text box appears.
4. Type Epinephrine (use capital 'E') and press ENTER. A molecule of epinephrine appears.

Note: *When you capitalize the molecule's name, ChemBio3D uses the substructures table to generate the structure, and the structure name appears in the model explorer. Otherwise, Name>Struct generates the structure and 'fragment1' appears.*

5. Click in the model window again to open another text box.
6. In the text box, Replace the word Epinephrine with Methamphetamine and press ENTER.

`Methamphetamine` appears in the model explorer.

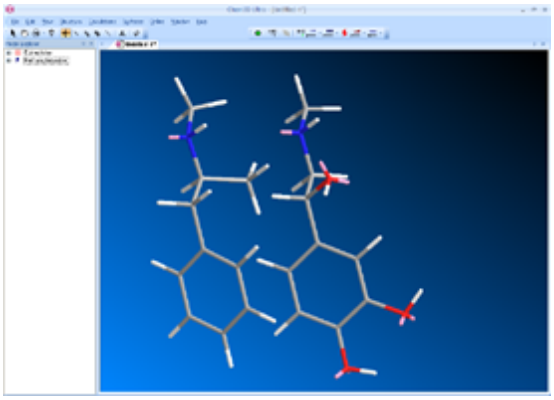


Figure 9.16: Two fragments.

If the two fragments are jumbled together, consider separating them so that the overlay results are clear.
To move one of the fragments:

1. Click the fragment name in the model explorer.
2. Using the Move Objects tool, click-drag the fragment in the model window.

To overlay the fragments:

1. Using the Move Objects tool, click an empty region of the model window to deselect all fragments.
2. In the model explorer window, click the epinephrine fragment to select it.
3. Right-click the fragment in the model explorer and go to **Overlay>Set Target Fragment**. The fragment is selected as the target.

Note: *To deselect a fragment as the target, go to* ***Overlay>Clear Target Fragment****.*

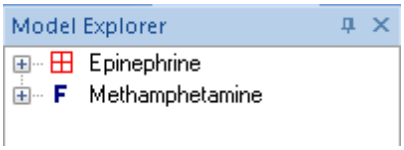


Figure 9.17: Model explorer with target selected.

4. In the model explorer window, right-click the methamphetamine fragment.
5. Go to **Overlay**>**fast overlay** on the context menu. The fragments are overlaid.

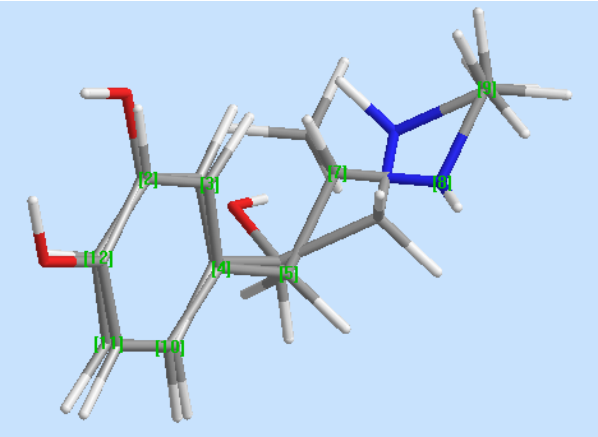


Figure 9.18: Overlaid fragments.

Tutorial 7: Aligning Models

The **Align** command lets you position a fragment in a desired orientation and proximity relative to a second fragment. Each fragment remains rigid during the alignment computation.
The Align command is available when two or more distances between atoms in one fragment and atoms in a second fragment are specified. These distances are entered into the Optimal field in the Measurement table.
You can use alignment to simulate the association of regions of similar lipophilicity and hydrophilicity on two proximate polymer chains.
In this tutorial, we demonstrate the Align command using two polymer chains.

Build the first polymer chain

1. Open a new Model window and select the Build from Text tool .
2. Click in the model window. A text box appears.
3. Type (AA-mon)3(C2F4)4(AA-mon)3H in the text box.
4. Press ENTER.

A polyacrylic acid/polytetrafluoroethylene block copolymer appears in the model window. The text, (AA-mon)3, is converted to a polymer segment with three repeat units of acrylic acid. The text, (C2F4)4, is converted to a polymer segment with four repeat units of tetrafluoroethylene.

Build a copy of the chain

Click in the model window well above and to the right of the first model. When the filled text box appears, press ENTER. A second polymer molecule appears.

Orient the chains

1. Click in the empty space in the model window to de-select any atoms in the model window.

2. Click the down arrow on the Rotate tool to open the rotation dial tool.
3. Select the **Y** axis, and drag the dial to show 55°.

Tip: *To get exactly 55° you may need to edit the value in the number box. After editing, press ENTER . The value displayed in the right corner of the dial should be the same as in the number box.*

The resulting model appears as shown below (the second model may appear in a different position on your computer):

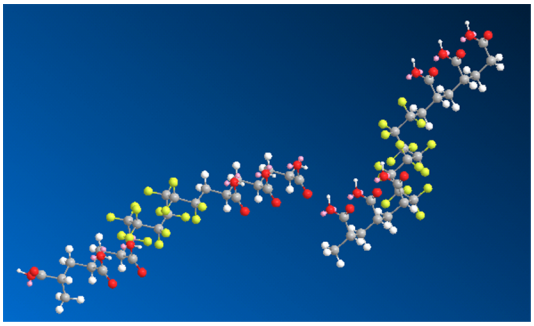


Figure 9.19: Aligning models.

Set optimal distances

The **Optimal** distance determines how closely the molecules align. In this tutorial, you will set the distance to 5Å.

1. In the model explorer, select **C(6)** in Fragment1 in the **AA-mon 2** group.
2. Locate the **C(98)** atom in Fragment 2 (**AA-mon 12** group) and CTRL+click to select it.
3. Go to **Structure**>**Measurements**>**Display Distance Measurement**.

The **C(98)-C(6)** atom pair appears in the measurement table.

4. Click the Optimal cell.
5. Type 5 and press ENTER.

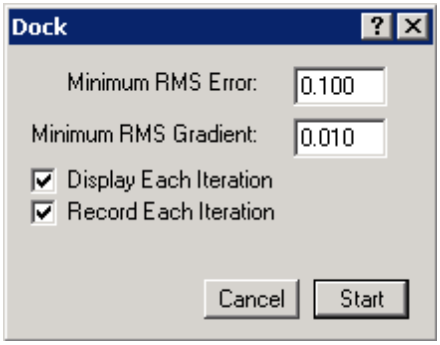
The optimal distance between C(6) and C(98) is specified as 5.000Å.
To have a reasonable align, you must specify *at least four atom pairs*. Repeat steps 1 through 5 for matching atom pairs throughout the fragments. For example, if you choose one pair from each group your list might look like this: Note that the Actual values in the following table may differ.

Atoms	Actual	Optimal
C(1)-C(93)	21.2034	5.0000
C(98)-C(6)	21.1840	5.0000

Atoms	Actual	Optimal
C(104)-C(12)	21.2863	5.0000
C(108)-C(16)	21.1957	5.0000
C(22)-C(114)	20.6472	5.0000
C(28)-C(120)	20.7001	5.0000
C(34)-C(126)	20.1410	5.0000
C(133)-C(41)	20.3559	5.0000
C(45)-C(137)	20.3218	5.0000
C(50)-C(142)	20.4350	5.0000

The distances in the Actual cell may differ because they depend on how the second polymer was positioned relative to the first polymer when the second polymer was created.
To begin the alignment computation:

1. Go to **Structure**>**Align**. The Align dialog box appears.
2. Type 0.100 for the **Minimum RMS Error** value and 0.010 for the **Minimum RMS Gradient**.



The docking computation stops when the RMS Error or the RMS Gradient becomes less than the Minimum RMS Error and Minimum RMS Gradient value.

3. Click **Display Each Iteration**.

This lets you see how much the fragments have moved after each iteration of the docking computation.

4. Click **Start**.

Note that while the alignment computation proceeds, one molecule remains stationary and the second molecule moves.

To stop the alignment computation before it reaches its preset RMS values, click **Stop Calculation** on the Calculation toolbar. Alignment and recording are stopped. The status bar displays the values describing each iteration. The illustration below shows the distances between atom pairs at the completion of the alignment computation. The distances in the Actual cell are close to the distances in the Optimal cell.

Measurement

	Display	Atoms	Actual (° / Å)	Optimal (° / Å)
1	☑	C(6)-C(98)	6.1484	5.0000
2	☑	C(1)-C(93)	6.0991	5.0000
3	☑	C(12)-C(104)	5.1307	5.0000
4	☑	C(16)-C(108)	4.6254	5.0000
5	☑	C(22)-C(114)	4.3976	5.0000
6	☑	C(28)-C(120)	4.1512	5.0000
7	☑	C(34)-C(126)	4.7687	5.0000
8	☑	C(41)-C(133)	5.1487	5.0000
9	☑	C(137)-C(45)	5.4206	5.0000
10	☑	C(50)-C(142)	6.0719	5.0000

Figure 9.20: Measurements for docked polymers.

Your results may not match those described here. The relative position of the two fragments or molecules at the start of the docking computation can affect results. For more accurate results, lower the minimum RMS gradient.

Tutorial 8: Viewing Orbitals

The highest occupied molecular orbitals (HOMO) and lowest unoccupied molecular orbitals (LUMO) are commonly the most important orbitals affecting molecular reactivity. This tutorial examines the orbitals of double bonds by looking at ethylene, the simplest molecule containing a double bond.

1. Go to **File**>**New**.
2. Build a model of ethene.
3. Go to **Calculations**>**Extended Hückel**>**Calculate Surfaces**.

The Highest Occupied Molecular Orbital (HOMO) is displayed by default. To view the HOMO:

1. Go to **Surfaces**>**Choose Surface**>**Molecular Orbital**.
2. Go to **Surfaces**>**Select Molecular Orbital** to see the HOMO/LUMO options. Select **HOMO (N=6)**. The pi bonding orbital surface appears.

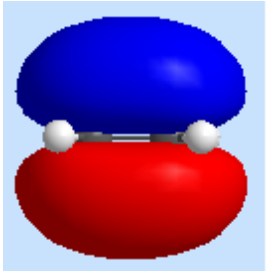


Figure 9.21: Pi bonding orbital surface.

Note: *You may need to rotate the molecule to view the orbitals.*

3. To view the LUMO, go to **Surfaces>Select Molecular Orbital** and Select **LUMO (N=7)**. The pi antibonding orbital surface appears.

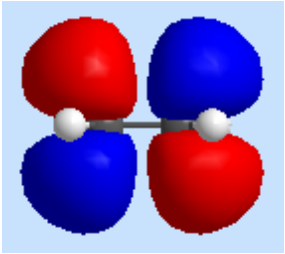


Figure 9.22: Pi antibonding orbital surface.

Tutorial 9: Mapping Surfaces

This tutorial demonstrates Gaussian minimization[1] and how to map calculated values to molecular surfaces for viewing. You can perform the same minimization using extended Hückel calculations.
The allyl radical is a simple example of resonance-enhanced stabilization.

Figure 9.23: The allyl radical.

To examine radicals with spin density surfaces, first create the allyl radical:

1. Go to **File>New**.
2. Right-click in an empty area of the ChemDraw panel (go to **View > ChemDraw Panel**, if it is hidden) and go to **Structure>Convert Name to Structure**.
3. In the Insert Structure text box, type 1-propene and click **OK**. A molecule of 1-propene appears.
4. In the Model window, select the H9 hydrogen using the Select tool .
5. Press DELETE.

   A dialog box appears asking if you want to turn off rectification. ChemBio3D knows that, or this valency, carbon atoms have four substituents.
6. Click **Turn Off Automatic Rectification**. The propene radical appears.

[1]Gaussian is available only for ChemBio3D Ultra.

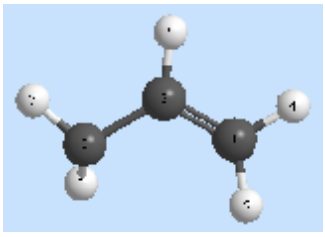


Figure 9.24: Propene radical model.

Next, perform the minimization:

1. Go to **Calculations**>**Gaussian Interface**>**Minimize (Energy/Geometry)**.
2. In the **Routine** tab, set the method to **PM3**, and the wave function to **U-Unrestricted Open-Shell**.
3. Set the **Wave Function** to **U-Unrestricted Open-Shell**.
4. Also in the **Routine** tab, set the **Spin Multiplicity** to **2**.

A spin multiplicity of 2 is required because the molecule is a radical.
One of the best ways to view spin density is by mapping it onto the Total Charge Density surface. This lets you see what portions of the total charge are contributed by unpaired electrons, or radicals.
To view spin density mapped onto the total charge density surface:

1. In the **Properties** tab, select **Molecular Surfaces** and **Spin Density**.
2. Click **Run**.

When the calculation is finished, select the Rotate tool and rotate the model back and forth. It should be completely planar.

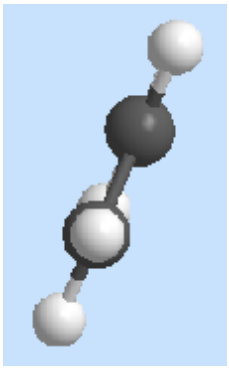


Figure 9.25: Viewing the minimized model.

To complete this tutorial, you need to adjust several surface settings. For convenience, activate the Surfaces toolbar. Go to **View**>**Toolbars**>**Surfaces**.

1. On the Surfaces toolbar, click **Surface**, and select **Total Charge Density**. The icon changes to denote the surface selected.
2. On the Surfaces toolbar, click **Display Mode**, and choose **Translucent**.
3. On the Surfaces toolbar, click **Color Mapping**, and choose **Spin Density**.
4. On the Surfaces toolbar, choose **Isocharge**. The Isocharge tool appears.

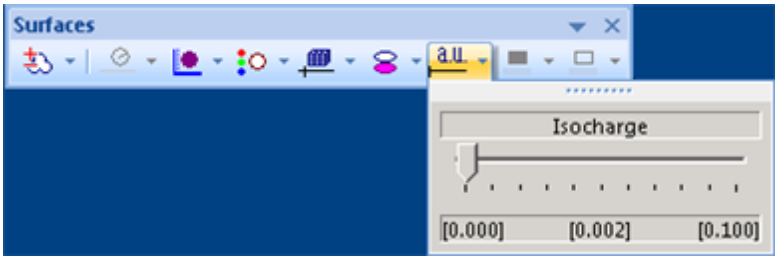


Figure 9.26: Using the Isocharge tool.

5. Set the isocharge to 0.050. (The number in the middle is the current setting.)

Note: *The isocharge is used to generate the surface. You can adjust this value to get the display you want. The illustration below was made with the setting of 0.0050.*

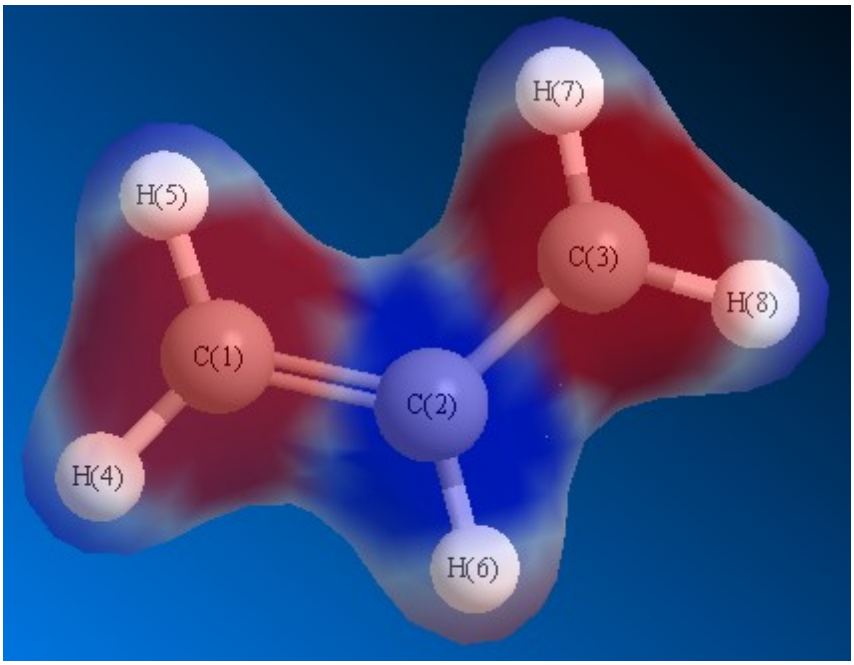


Figure 9.27: Viewing the total charge density surface.

Most of the surface is gray, indicating that there is no contribution to it from unpaired electrons. The areas of red centered over the terminal carbons is a visual representation of the expected delocalization of the radical—there is some radical character simultaneously on both of these carbons.

Now, toggle the surface off by clicking the Surfaces icon .

Spin Density

Here we determine the raw spin density alone, not mapped onto the charge density surface.

1. On the Surfaces toolbar, point to **Surface**, and select **Total Spin Density**.
2. Go to **Surfaces**>**Display Mode**>**Wire Mesh**.
3. Set Isospin to 0.001.

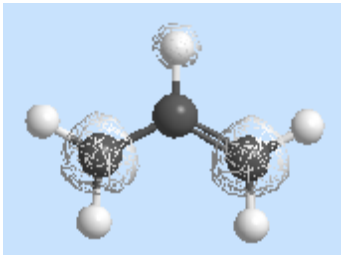


Figure 9.28: Wire mesh surfaces.

There is a large concentration of unpaired spin over each of the terminal carbons and a small concentration over the central hydrogen. This small amount of spin density is not very significant—you could not even see it when looking at the mapped display earlier, but the calculations show that it is, in fact, there.

Tutorial 10: Partial Charges

Each atom of a molecule contributes an integral charge to the molecule as a whole. This integral contribution is known as the formal charge of the atom.

To compute the integral charge of a molecule, the number of electrons contributed by each of its atoms can be subtracted from the number of protons in the nucleus of each of its atoms.

In ChemBio3D, some atoms have non-integral delocalized charges. For example, the two oxygen atoms in nitrobenzene each have charges of -0.5 because there is one electron shared across the two N-O bonds. For more accuracy, quantum mechanics calculations can produce partial charges (which are also non-integral).

However, as shown in Tutorial 9, electrons in molecules actually occupy areas of the molecule that are not associated with individual atoms and can also be attracted to different atomic nucleii as they move across different atomic orbitals. In fact, bonds are a representation of the movement of these electrons between different atomic nucleii.

Because electrons do not occupy the orbitals of a single atom in a molecule, the actual charge of each atom is not integral, but is based on the average number of electrons in the model that are occupying the valence shells of that atom at any given instant. By subtracting this average from the number of protons in the molecule, the partial charge of each atom is determined.

Visualizing the partial charge of the atoms in a molecule is another way to understand the model's reactivity. Typically the greater the partial charge on an atom, the more likely it is to form bonds with other atoms whose partial charge is the opposite sign.

Note: *ChemBio3D recognizes formal charges you assign to atoms in the model window and ChemDraw panel. It then calculates delocalized charges for all atoms in the model where delocalization occurs. To display formal and delocalized charges, hover the mouse over a charged atom.*

Using the theories in Extended Hückel, CS MOPAC, or Gaussian, you can compute the partial charges for each atom. In the following example, the partial charges for phenol are computed by Extended Hückel.

1. Go to the **File**>**New**.
2. Using the Text Building tool, click in the model window.
3. Type PhOH in the text box, and press ENTER . A molecule of phenol is created.
4. To compute Extended Hückel charges, go to **Calculations**>**Extended Hückel**>**Calculate Charges**.

The Atom Property table opens, displaying the results. To view the table at any time, go to **View**>**Atom Property Table**.

Displaying Partial Charges

You can use gradient colors to illustrate partial charges for atoms in your model. For example, strongly positive charged atoms may appear bright red while strongly negative atoms appear blue. Lesser positively and negatively charged atoms also appear somewhere within the color range, depending on the value. To display partial charges, you first need to run the charge calculation.

To display partial charges:

1. Go to **File**>**Model Settings** and select the **Colors & Fonts** tab.
2. Under **Color by**, select **Atom Properties**.
3. In the Atom Properties drop-down list, select **Charge(Hückel)**.
4. Select one of the two color bands. The first band ranges from blue to red. The second band has a more refined range of color.
5. In the **min**/**max** text boxes, select the range of calculations you want to colorize. To select the entire range of values calculated for the model, click **Scan Value Range**.
6. To view the model with your options, select the **Preview** check box at the bottom of the dialog box and click **Apply**.
7. Click **OK**.

All the atoms are colored according to the color scale you chose. Atoms with a large negative partial charge are deep blue. Atoms with a large positive partial charge are deep red. As the magnitude of the charges approaches 0, the color of the atom becomes paler.

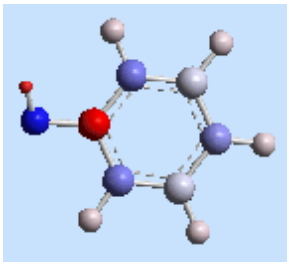


Figure 9.29: Partial charges for phenol.

For phenol, the greatest negative charge is on the oxygen atom. The greatest positive charge is on the adjacent carbon atom (with the adjacent hydrogen atom a close second). The rest of the molecule has relatively pale atoms; their partial charges are much closer to zero.

Before starting the tutorials, we recommend that you choose the default settings and an appropriate display so that your results are similar to what you see in this guide.

To use the default settings:

1. Go to **File**>**Model Settings**.
2. In the Model Settings dialog box, click **Reset to Default**.
3. Click **OK**.

To view models as shown in these tutorials:

1. Go to **View**>**Toolbars**>**Model Display**.
2. On the **Model Display** toolbar, select the **Display Mode** drop-down list and choose **Cylindrical Bonds**.

Using calculation engines

Tutorial 11: Rotamer Analysis

In this tutorial we use GAMESS to identify the preferred (lowest energy) conformer around a specified bond in a simple molecule. To identify the conformer, we run conformational analysis on the molecule and then perform a GAMESS minimization calculation on each of two of its conformers, one above a local energy minimum and another above the global energy minimum. We then compare the results of the calculations.

We will use 2-phenylethanimine as the molecule. For the purpose of this tutorial, we will number the atoms as shown below:

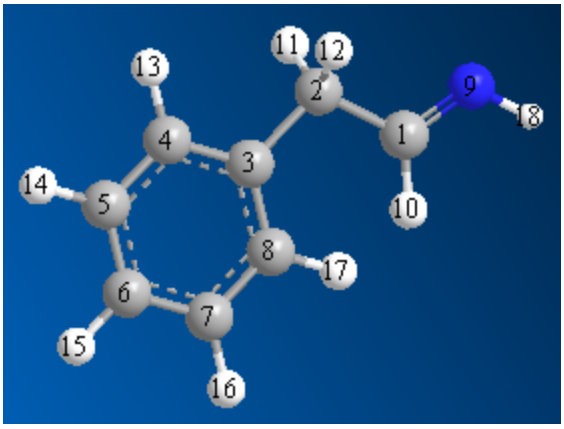


Figure 9.30: 2-phenylethanimine.

We need to select the desired bond and run a conformational analysis on it that will be used in both GAMESS minimizations. For this tutorial, we will choose the bond shown in red below:

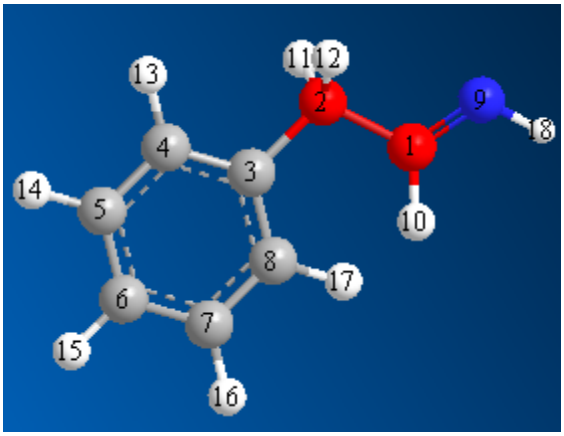


Figure 9.31: The C(1)-C(2) bond appears in red.

When analyzing the conformers of a bond, you can set the angles of other bonds as desired. For this tutorial, we will set the C(1)-C(2)-C(3)-C(4) dihedral bond angle to 90 degrees as follows:

1. In the ChemDraw panel, draw 2-phenylethanimine. The molecule appears in the model window.
2. Go to **Structure**>**Measurements**>**Generate All Dihedral Angles**. The Measurement table appears.
3. In the Measurement table, select the C(1)-C(2)-C(3)-C(4) bond.
4. In the `Actual` column, change the angle for the C(1)-C(2)-C(3)-C(4) bond to 90 degrees and press ENTER.

Now that the dihedral bond is set, we will run the conformation around the C(1)-C(2) bond.
To run the conformation analysis:

5. In the model window, select the C(1)-C(2) bond using the Move Objects tool.

6. To run the conformation analysis, go to **Calculations**>**Dihedral Driver**>**Single Angle Plot**. The Dihedral Driver Chart opens, displaying the conformational energy for the C(1)-C(2) bond.

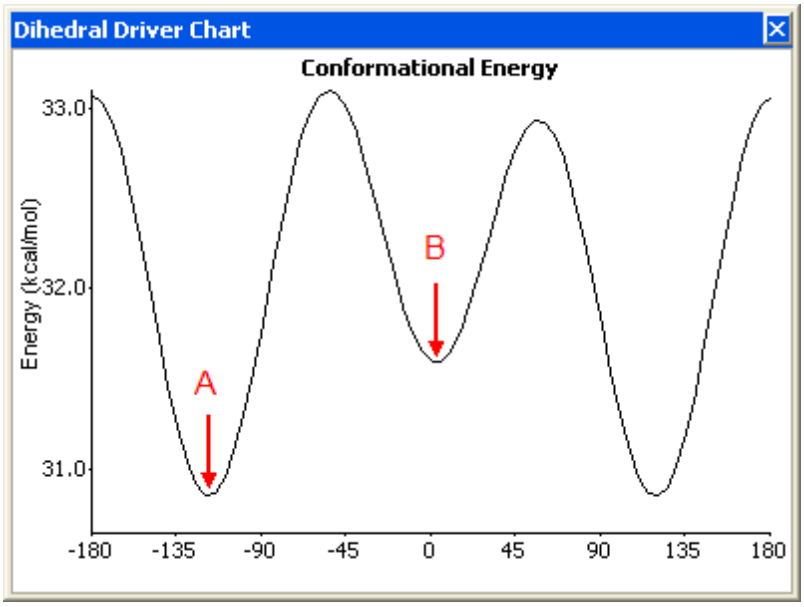


Figure 9.32: Dihedral chart for the C(1)-C(2) bond in 2-phenylethanimine. The arrows indicate A) the global minimum conformation and B) a local minimum conformation.

We now select two conformers and run the GAMESS minimization on each one. We start by selecting a conformer that is above the global minimum.

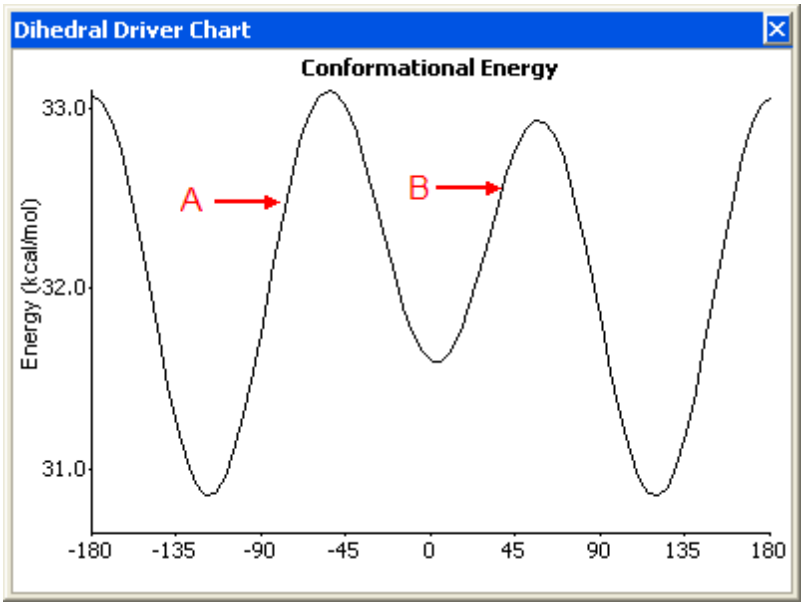


Figure 9.33: The dihedral chart with the conformer positions shown. We select point A to calculate the global minimum and point B to calculate a local minimum.

To run a GAMESS minimization above the global minimum:

1. In the Dihedral Chart, click a point above the global minimum (for example, point A in the figure above).
2. Go to **Calculations**>**GAMESS Interface**>**Minimize**. The GAMESS Interface dialog box opens.
3. In the dialog box, click **Run**.

The global minimum energy appears in the Output window (approximately -226273 Kcal/Mol).
To run a GAMESS minimization above a local minimum:

1. In the Dihedral Chart, click a point above a local minimum (for example, point B in the figure above).
2. Go to **Calculations**>**GAMESS Interface**>**Minimize**. The GAMESS Interface dialog box opens.
3. In the dialog box, click **Run**.

For the local minimization, the result is approximately -226270 Kcal/Mol.
The preferred conformer is lower by about 3 Kcal/Mol.

Tutorial 12: Calculating Rotational Bonds

In this tutorial, we illustrate how to calculate the rotational energy of a C-C bond in biphenyl using the dihedral driver. We run the dihedral driver twice--first, with the minimization energy turned on and then with the minimization energy turned off.

Building biphenyl

We first need to build a model of biphenyl. The easiest way is to use Name>Struct:

1. With the text tool selected, click in the model window. A text field appears.
2. In the text field, type `biphenyl` and press ENTER. A model of biphenyl appears.

Calculating the dihedral driver

The dihedral driver lets you map the conformational space of a model by varying either one or two dihedral angles (we use one in this tutorial). With minimization turned on, the model energy is minimized at each dihedral angle value using the MM2 force field and the total energy of the model is calculated and graphed. After the calculation is complete, you can view the data to locate the models with the lowest energy values and use these as starting points for further refinement in locating a stationary point.
To turn on the minimization:

1. Go to **File**>**Preferences**.
2. In the Preferences window, select the **Dihedral Driver** tab.
3. Select the **Enable Minimization** checkbox.
4. Click **OK**.

For the dihedral driver calculation, you must select a bond in your model. For this tutorial, we select the C-C bond between the benzene rings.

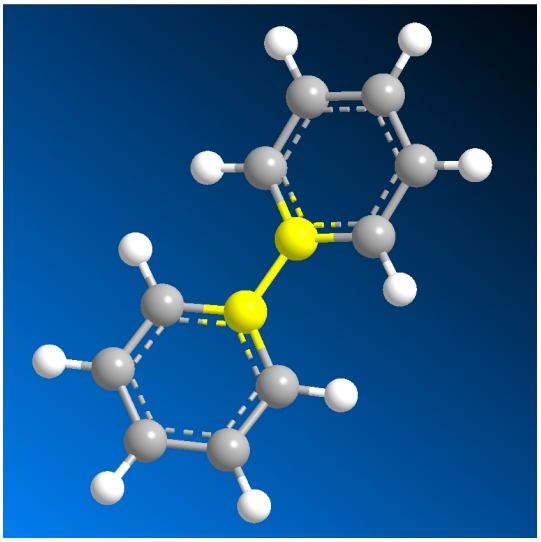


Figure 9.34: A biphenyl model with the C-C bond selected.

To calculate the rotational bond energy:

1. Using the selection tool, click the C-C bond between the rings.
2. Go to **Calculations**>**Dihedral Driver**>**Single Angle Plot**. The calculation begins.

During the calculation, the model window displays the model being rotated around the selected bond while the Output window reports the energy value at each incremental angle.

Examining the lowest /highest energies

When the calculation is complete, the Dihedral Driver Chart opens, displaying a graph of the energy (in kcal) versus the angle of rotation around the C-C bond (the same data appears in the Output window).
To view the conformation at any given point:

1. In the chart, click any location along the curve. The model display rotates the dihedral to the selected conformation.
2. To see the conformation energy through a range of rotation angles, click and drag across the chart while viewing the model.

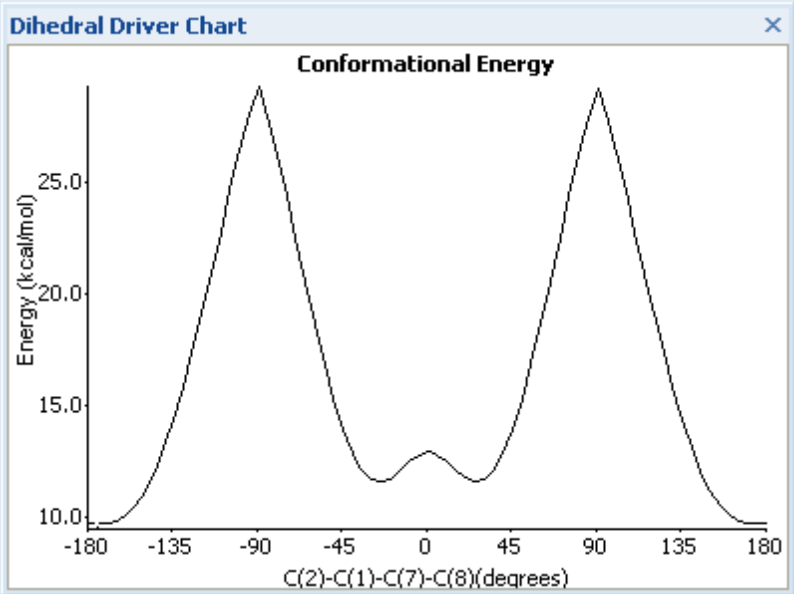


Figure 9.35: Single angle plot of the diphenyl C-C bond with minimization turned on.

The dihedral rotates in 5-degree increments through 360 degrees for a total of 72 conformations to produce the graph. You can view the minimized energy values for each point in the Output window.

***Tip:** To rotate the other dihedral angle (other end of the bond), right-click in the Dihedral Driver Chart and choose **Rotate other End**.*

Repeating the calculation

We now need to turn the minimization off and repeat the calculation. Right-click the chart and select **Recompute without Minimization**. This chart appears:

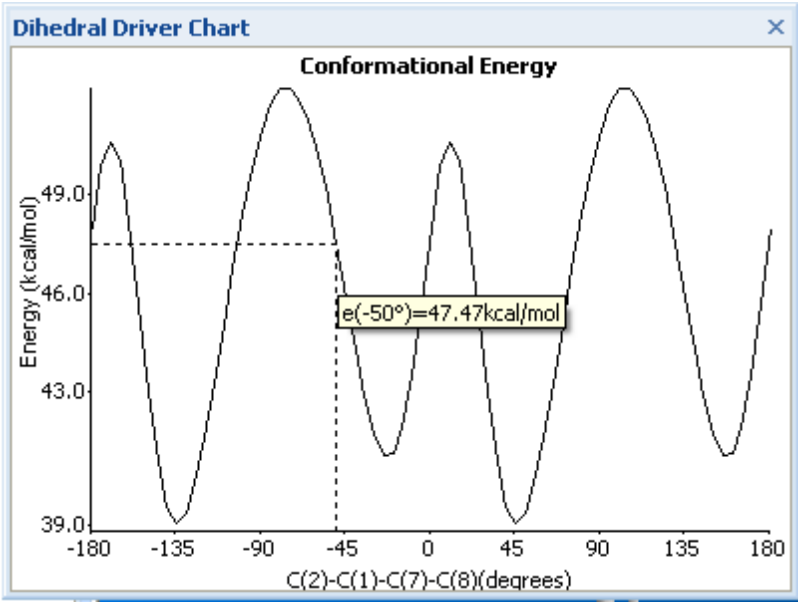


Figure 9.36: Single angle plot of the diphenyl C-C bond with minimization turned off.

Customizing the Dihedral Driver Chart

By default, the dihedral chart displays data in 5-degree increments. To change this increment, go to **File**>**Preferences**, and select the **Dihedral Driver** tab in the Preferences dialog box.

To customize the colors used in the chart, select the color options in the Chart colors drop-down lists.

Computation Concepts

Computational chemistry overview

Computational chemistry lets you explore molecules using a computer when a laboratory investigation may be inappropriate, impractical, or impossible.

Aspects of computational chemistry include:

- Molecular modeling.
- Computational methods.
- Computer-Aided Molecular Design (CAMD).
- Chemical databases.
- Organic synthesis design.

Molecular modeling can be thought of as the rendering of a 2D or 3D model of a molecule's structure and properties. Computational methods, on the other hand, calculate the structure and property data necessary to render the model. Within a modeling program such as ChemBio3D, computational methods are referred to as computation engines, while geometry engines and graphics engines render the model.

ChemBio3D supports several powerful computational chemistry methods and extensive visualization options.

Computational methods overview

Computational chemistry encompasses a variety of mathematical methods which fall into two broad categories:

- **Molecular mechanics**: Applies the laws of classical physics to the atoms in a molecule without explicit consideration of electrons.
- **Quantum mechanics**: Relies on the Schrödinger equation to describe a molecule with explicit treatment of electronic structure.

Quantum mechanical methods can be subdivided into two classes: *Ab initio* and Semi-empirical.

ChemBio3D provides these methods:

Method		
molecular mechanics	▪ MM2 ▪ MM3, MM3-protein	ChemBio3D 13.0, Tinker
Semi-empirical	▪ extended Huckel ▪ other semi-empirical methods (AM1, MINDO/3, PM3, etc.)	ChemBio3D 13.0, MOPAC, Gaussian
Ab initio	▪ RHF, UHF, MP2, etc.	Gaussian, CS GAMESS

Figure 10.1: Computational Chemistry Methods.

- Molecular mechanical methods: MM2 (directly). MM3 and MM3-protein through the ChemBio3D 13.0 Tinker interface.
- Semi-empirical Extended Hückel, MINDO/3, MNDO, MNDO-d, AM1 and PM3 methods through ChemBio3D and Gaussian.
- *Ab initio* methods through the ChemBio3D Gaussian or CS GAMESS interface.

Uses of computational methods

Computational methods calculate the Potential Energy Surfaces (PES) of molecules. The potential energy surface is the embodiment of the forces of interaction among atoms in a molecule. From the PES, structural and chemical information about a molecule can be derived. The methods differ in the way the surface is calculated and in the molecular properties derived from the energy surface.

The methods perform the following basic types of calculations:

- **Single point energy calculation**: The energy of a given geometry of the atoms in a model which is the value of the PES at that point.
- **Geometry optimization**: A systematic modification of the atomic coordinates of a model resulting in a geometry where the forces on each atom in the structure is zero. A 3-dimensional arrangement of atoms in the model representing a local energy minimum (a stable molecular geometry to be found without crossing a conformational energy barrier).
- **Property calculation**: Predicts certain physical and chemical properties, such as charge, dipole moment, and heat of formation.

Computational methods can perform more specialized functions, such as conformational searches and molecular dynamics simulations.

Geometry optimization

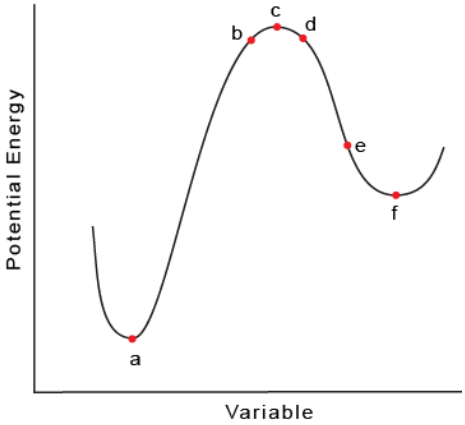
Before performing calculations on your model, you may want to optimize its geometry by determining its stable conformations.

You can find the stable conformations by performing energy minimization calculations. These calculations determine the model's local and global energy minima.

Geometry optimizations are iterative and begin at some starting geometry as follows:

1. You first perform a single point energy calculation on the starting geometry.
2. you change the coordinates for some subset of atoms and perform another single point energy calculation to determine the energy of that new conformation. The first or second derivative of the energy (depending on the method) with respect to the atomic coordinates determines how large and in what direction the next increment of geometry change should be.
3. The change is made.
4. Following the incremental change,ChemBio3D again determines the energy and energy derivatives and the process continues until convergence is achieved, at which point the minimization process terminates.

The accuracy of the energy minimization calculations depends on the starting geometry, the potential energy function used, and the settings for a minimum acceptable gradient between steps (convergence criteria).
The following illustration shows some concepts of minimization. For simplicity, this plot shows a single independent variable plotted in two dimensions.



The starting geometry of the model determines which minimum is reached. For example, starting at (b), minimization results in geometry (a), which is the global minimum. Starting at (d) leads to geometry (f), which is a local minimum.The proximity to a minimum, but not a particular minimum, can be controlled by specifying a minimum gradient that should be reached. Geometry (f), rather than geometry (e), can be reached by decreasing the value of the gradient where the calculation ends.
In theory, if a convergence criterion (energy gradient) is too lax, a first-derivative minimization can result in a geometry that is near a saddle point. This occurs because the value of the energy gradient near a saddle point, as near a minimum, is very small. For example, at point (c), the derivative of the energy is 0, and as far as the minimizer is concerned, point (c) is a minimum. First derivative minimizers cannot, as a rule, cross saddle points to reach another minimum.

Note: *If the saddle point is the extremum of interest, it is best to use a procedure that locates a transition state, such as the CS MOPAC Optimize To Transition State command.*

You can take these steps to ensure that a minimization has not resulted in a saddle point.

- Slightly alter the geometry and perform another minimization. The new starting geometry might result in either (a), or (f) in a case where the original geometry led to (c).
- Apply the dihedral driver to search the conformational space of the model. See "Tutorial 5: The Dihedral Driver " on page 179.
- Run a molecular dynamics simulation, which allows small potential energy barriers to be crossed. After completing the molecular dynamics simulation, you can then minimize and analyze individual geometries. See "MM2 references" on page 291.

You can calculate these properties with the computational methods available through ChemBio3D using the PES:

- Steric energy
- Heat of formation

- Dipole moment
- Charge density
- COSMO solvation in water
- Electrostatic potential
- Electron spin density
- Hyperfine coupling constants
- Atomic charges
- Polarizability
- Others, such as IR vibrational frequencies

Choosing the best method

Not all types of calculations are possible for all methods and no one method is best for all purposes. For any given application, each method poses advantages and disadvantages. The choice of method depends on a number of factors, including:

- The nature and size of the molecule
- The type of information sought
- The availability of applicable experimentally determined parameters (as required by some methods)
- Computer resources

The three most important criteria are:

- **Model size**: The size of a model can be a limiting factor for a particular method. The limiting number of atoms in a molecule increases by approximately one order of magnitude between method classes from *ab initio* to molecular mechanics. A*b initio* is limited to tens of atoms, semiempirical to hundreds, and molecular mechanics to thousands.
- **Parameter Availability**: Some methods depend on experimentally determined parameters to perform computations. If the model contains atoms for which the parameters of a particular method have not been derived, that method may produce invalid predictions. Molecular mechanics, for example, relies on parameters to define a force-field. A force-field is only applicable to the limited class of molecules for which it is parametrized.
- **Computer resources**: Requirements increase relative to the size of the model for each of the methods.

  Ab initio: The time required for performing computations increases on the order of N^4, where N is the number of atoms in the model.
  Semiempirical: The time required for computation increases as N^3 or N^2, where N is the number of atoms in the model.
  MM2: The time required for performing computations increases as N^2, where N is the number of atoms.

In general, molecular mechanical methods are computationally less expensive than quantum mechanical methods. The suitability of each general method for particular applications can be summarized as follows.

Molecular mechanics methods

Molecular mechanics in ChemBio3D 13.0 apply to:

- Systems containing thousands of atoms.

- Organic, oligonucleotides, peptides, and saccharides.
- Gas phase only (for MM2).

Useful techniques available using MM2 methods include:

- Energy Minimization for locating stable conformations.
- Single point energy calculations for comparing conformations of the same molecule.
- Searching conformational space by varying one or two dihedral angles.
- Studying molecular motion using Molecular Dynamics.

Quantum mechanical methods

Useful information determined by quantum mechanical methods includes:

- Molecular orbital energies and coefficients.
- Heat of Formation for evaluating conformational energies.
- Partial atomic charges calculated from the molecular orbital coefficients.
- Electrostatic potential.
- Dipole moment.
- Transition-state geometries and energies.
- Bond dissociation energies.

Semiempirical methods available in ChemBio3D 13.0 with Gaussian apply to:

- Systems containing up to 120 heavy atoms and 300 total atoms.
- Organic, organometallics, and small oligomers (peptide, nucleotide, saccharide).

Gas phase or implicit solvent environment.

- Ground, transition, and excited states.

Ab initio methods available in ChemBio3D 13.0 with Gaussian apply to:

- Systems containing up to 150 atoms.
- Organic, organometallics, and molecular fragments (catalytic components of an enzyme).
- Gas or implicit solvent environment.
- Study ground, transition, and excited states (certain methods).

Method Type	Advantages	Disadvantages	Best For
Molecular Mechanics (Gaussian) Uses classical physics Relies on force-field with embedded empirical parameters	Least intensive computationally—fast and useful with limited computer resources Can be used for molecules as large as enzymes	Particular force field applicable only for a limited class of molecules Does not calculate electronic properties Requires experimental data (or data from *ab initio*) for parameters	Large systems (thousands of atoms) Systems or processes with no breaking or forming of bonds
Semiempirical (MOPAC, Gaussian) Uses quantum physics Uses experimentally derived empirical parameters Uses approximation extensively	Less demanding computationally than *ab initio* methods Capable of calculating transition states and excited states	Requires experimental data (or data from *ab initio*) for parameters Less rigorous than *ab initio* methods	Medium-sized systems (hundreds of atoms) Systems involving electronic transitions
ab initio (Gaussian, CS GAMESS) Uses quantum physics Mathematically rigorous—no empirical parameters	Useful for a broad range of systems Does not depend on experimental data Capable of calculating transition states and excited states	Computationally intensive	Small systems (tens of atoms) Systems involving electronic transitions Molecules or systems without available experimental data ("new" chemistry) Systems requiring rigorous accuracy

Figure 10.2: Comparison of Methods.

Potential energy surfaces

A potential energy surface (PES) can describe:

- A molecule or ensemble of molecules having constant atom composition (ethane, for example) or a system where a chemical reaction occurs.
- Relative energies for conformations (eclipsed and staggered forms of ethane).

Potential energy surfaces can differentiate between:

- Molecules having slightly different atomic composition (ethane and chloroethane).
- Molecules with identical atomic composition but different bonding patterns, such as propylene and cyclopropane
- Excited states and ground states of the same molecule.

The true representation of a model's potential energy surface is a multi-dimensional surface whose dimensionality increases with the number of atom coordinates. Since each atom has three independent variables (x, y, z coordinates), visualizing a surface for a many-atom model is impossible. However, you can generalize this problem by examining any two independent variables, such as the x and y coordinates of an atom.
The main areas of interest on a potential energy surface are the extrema, as indicated by the arrows:

- **Global minimum**: The most stable conformation appears at the extremum where the energy is lowest. A molecule has only one global minimum.
- **Local minima**: Additional low energy extrema. Minima are regions of the PES where a change in geometry in any direction yields a higher energy geometry.
- **Saddle point**: A stationary point between two low energy extrema. A saddle point is defined as a point on the potential energy surface at which there is an increase in energy in all directions except one, and for which the slope (first derivative) of the surface is zero.

Note: *At the energy minimum, the energy is not zero; the first derivative (gradient) of the energy with respect to geometry is zero.*

All the minima on a potential energy surface of a molecule represent stable stationary points where the forces on each atom sums to zero. The global minimum represents the most stable conformation; the local minima, less stable conformations; and the saddle points represent transition conformations between minima.

Single point energy calculations

Single point energy calculations can be used to calculate properties of specific geometry of a model. The values of these properties depend on where the model lies on the potential surface as follows:

- A single point energy calculation at a global minimum provides information about the model in its most stable conformation.
- A single point calculation at a local minimum provides information about the model in one of many stable conformations.
- A single point calculation at a saddle point provides information about the transition state of the model.
- A single point energy calculation at any other point on the potential energy surface provides information about that particular geometry, not a stable conformation or transition state.

Single point energy calculations can be performed before or after optimizing geometry.

Note: *Do not compare values from different methods. Different methods rely on different assumptions about a given molecule, and the energies differ by an arbitrary offset.*

Molecular mechanics theory in brief

Molecular mechanics computes the energy of a molecule in terms of a set of classical potential energy functions. The potential energy functions and the parameters used for their evaluation are known as a "force-field".
Molecular mechanical methods are based on several principles:

- Nuclei and electrons are lumped together and treated as unified particles (atoms).
- Atoms are typically treated as spheres.
- Bonds are typically treated as springs.
- Non-bonded interactions between atoms are described using potential functions derived from classical mechanics.
- Individual potential functions are used to describe the different interactions: bond stretching, angle bending, torsion (bond twisting), and through-space (non-bonded) interactions.
- Potential energy functions rely on empirically derived parameters (force constants, equilibrium values) that describe the interactions between sets of atoms.
- The sum of the interactions determines the conformation of the molecule.
- Molecular mechanical energies *have no meaning as absolute quantities*. They can only be used to compare relative steric energy (strain) between two or more conformations of the same molecule.

The force-field

Since molecular mechanics treats bonds as springs, the mathematics of spring deformation (Hooke's Law) is used to describe the ability of bonds to stretch, bend, and twist. Non-bonded atoms (greater than two bonds apart) interact through van der Waals attraction, steric repulsion, and electrostatic attraction and repulsion. These properties are easiest to describe mathematically when atoms are considered as spheres of characteristic radii. The total potential energy, E, of a molecule can be described by:

E= Stretching energy + Bending energy + Torsion energy + Non-bonded interaction energy

The first three terms, the bonded interactions, can be viewed as a strain energy imposed by a model moving from some ideal zero strain conformation.
Stretching energy. bond stretching between directly bonded atoms.
Bending energy. angle bending between two atoms that are adjacent to a third atom.
Torsion energy. torsional angle rotation between atoms that form a dihedral angle.
Non-bonded interaction energy. The non-bonded interaction include these two forces:

- Repulsion for atoms that are too close and attraction at long range from dispersion forces (van der Waals interaction).
- Interactions from charges, dipoles, quadrupoles (electrostatic interactions).

This illustration shows the major interactions:

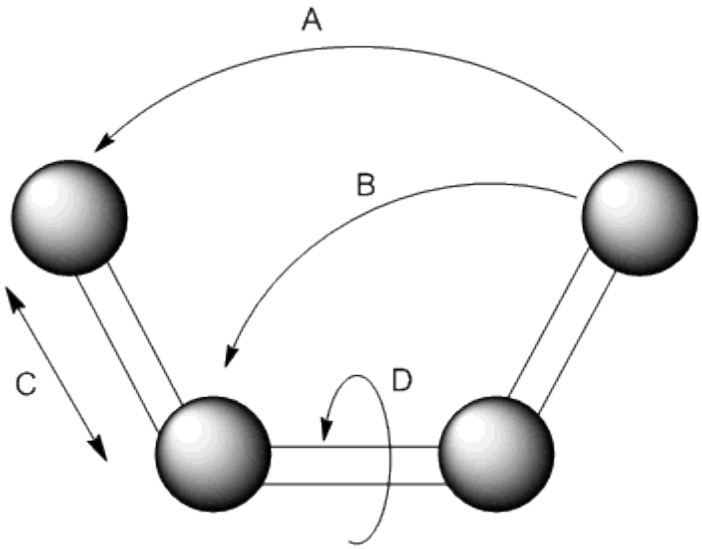


Figure 10.3: Potential Energy Interactions. A) non-bonded interactions; B) angle bending; C) bond stretching; D) torsion.

Different force-fields have been developed. Some include additional energy terms that describe other deformations (such as the coupling between bending and stretching in adjacent bonds) to improve the accuracy of the mechanical model.

MM2

ChemBio3D uses a modified version of Allinger's MM2 force field. For additional MM2 references see "MM2 references" on page 291.

The principal additions to Allinger's MM2 force field are:

- A charge-dipole interaction term
- A quartic stretching term
- Cutoffs for electrostatic and van der Waals terms with 5th order polynomial switching function
- Automatic pi system calculations when necessary
- Torsional and non-bonded constraints

ChemBio3D stores the parameters for the potential energy function in parameter tables. To view the tables, go to **View>Parameter Tables** and select one of the MM2 tables.

Each parameter is classified by a Quality number, which indicates the reliability of the data. The quality ranges from 4, where the data is derived completely from experimental data (or *ab initio* data), to 1, where the data is guessed by ChemBio3D.

The parameter table MM2 Constants contains adjustable parameters that correct for failings of the potential functions in outlying situations.

Caution: *Editing of MM2 parameters should only be done with the greatest of caution by expert users. Within a force-field equation, parameters operate interdependently; changing one normally requires that others be changed to compensate for its effects.*

Bond stretching energy

The bond stretching energy equation is based on Hooke's law:

$$E_{Stretch} = 71.94 \sum_{Bonds} K_s (r - r_o)^2$$

The parameters are stored in the Bond Stretching parameter table. Unique K_s and r_o parameters are assigned to each pair of bonded atoms based on their atom types (C-C, C-H, O-C). The K_s parameter controls the stiffness of the spring's stretching (bond stretching force constant), r_o defines its equilibrium length (the standard measurement used in building models). The constant, 71.94, is a conversion factor to obtain the final units as kcal/mole.
The result of this equation is the energy contribution associated with the deformation of the bond from its equilibrium bond length.
This simple parabolic model fails when bonds are stretched toward the point of dissociation. The Morse function would be the best correction for this problem. However, the Morse function significantly increases computation time. As an alternative, cubic stretch and quartic stretch constants are added to provide a result approaching a Morse-function correction.
The cubic stretch term allows for an asymmetric shape of the potential well, allowing these long bonds to be handled. However, the cubic stretch term is not sufficient to handle abnormally long bonds. A quartic stretch term is used to correct problems caused by these very long bonds. With the addition of the cubic and quartic stretch term, the equation for bond stretching becomes:

$$E_{stretch}=71.94\sum K_s[(r-r_0)^2+CS(r-r_0)^3+QS(r-r_0)^4]$$

Both the cubic and quartic stretch constants are defined in the MM2 Constants table.
To precisely reproduce the energies obtained with Allinger's force field, set the cubic and quartic stretching constant to "0" in the MM2 Constants tables.

Angle bending energy

$$E_{Bend} = 0.02191418 \sum_{Angles} K_b (\theta - \theta_o)^2$$

The bending energy equation is also based on Hooke's law. The K_b parameter controls the stiffness of the spring's bending (angular force constant), while θ_0 defines the equilibrium angle. This equation estimates the energy associated with deformation about the equilibrium bond angle. The constant, 0.02191418, is a conversion factor to obtain the final units as kcal/mole.

Unique parameters for angle bending are assigned to each bonded triplet of atoms based on their atom types (C-C-C, C-O-C, C-C-H). For each triplet of atoms, the equilibrium angle differs depending on what other atoms the central atom is bonded to. For each angle there are three possibilities: XR2, XRH or XH2. For example, the XH2 parameter would be used for a C-C-C angle in propane, because the other atoms the central atom is bonded to are both hydrogens. For isobutane, the XRH parameter would be used; for 2,2-dimethylpropane, the XR2 parameter would be used.

The effect of the K_b and θ_0 parameters is to broaden or steepen the slope of the parabola. The larger the value of K_b, the more energy is required to deform an angle from its equilibrium value. Shallow potentials are achieved with K_b values less than 1.0.

A sextic term is added to increase the energy of angles with large deformations from their ideal value. The sextic bending constant, SF, is defined in the MM2 Constants table. With the addition of the sextic term, the equation for angle bending becomes:

$$E_{Bend} = 0.02191418 \sum_{Angles} K_b[(\theta - \theta_o)^2 + SF(\theta - \theta_o)^6]$$

Note: *The default value of the sextic force constant is 0.00000007. To precisely reproduce the energies obtained with Allinger's force field, set the sextic bending constant to "0" in the MM2 Constants tables.*

There are three parameter tables for the angle bending parameters:

- Angle Bending parameters
- 3-Membered Ring Angle Bending parameters
- 4-Membered Ring Angle Bending parameters

There are three additional angle bending force constants available in the MM2 Constants table. These are the "-CHR- Bending" constants, specifically for carbons with one or two attached hydrogens.

The -CHR- Bending K_b for 1-1-1 angles[1] allows more accurate force constants to be specified for Type 1 (-CHR-) and Type 2 (-CHR-) interactions.

The -CHR-Bending K_b for 1-1-1 angles in 4-membered rings and the -CHR- Bending K_b for 22-22-22 angles in 3-membered rings require separate constants for accurate specification.

Torsion energy

$$E_{Twist} = \sum_{Torsions} \frac{V_n}{2}[1 + \cos(n\phi - \phi)]$$

[1]The numbers in the angle definitions refer to the **Text** column in the Atom Types Table. 1 refers to C-alkane, and 22 refers to C-cyclopropane.

This term accounts for the tendency for dihedral angles (torsionals) to have an energy minimum occurring at specific intervals of 360/n. In ChemBio3D, n can equal 1, 2, or 3.

$$E_{Twist} = \sum_{Torsions} \frac{V_1}{2}(1+\cos\phi) + \frac{V_2}{2}(1+\cos 2\phi) + \frac{V_3}{2}(1+\cos 3\phi)$$

The $V_n/2$ parameter is the torsional force constant. It determines the amplitude of the curve. The *n* signifies its periodicity. $n\phi$ shifts the entire curve about the rotation angle axis. The parameters are determined through curve-fitting techniques. Unique parameters for torsional rotation are assigned to each bonded quartet of atoms based on their atom types (C-C-C-C, C-O-C-N, H-C-C-H).
ChemBio3D provides three torsional parameters tables:

- Torsional parameters
- 4-Membered ring torsions
- 3-Membered ring torsions

Non-bonded energy

The non-bonded energy represents the pair-wise sum of the energies of all possible interacting non-bonded atoms within a predetermined “cut-off” distance.
The non-bonded energy accounts for repulsive forces experienced between atoms at close distances, and for the attractive forces felt at longer distances. It also accounts for their rapid falloff as the interacting atoms move farther apart by a few Angstroms.

van der Waals energy

Repulsive forces dominate when the distance between interacting atoms becomes less than the sum of their contact radii. In ChemBio3D, repulsion is modeled by an equation which combines an exponential repulsion with an attractive dispersion interaction (1/R6):

$$E_{van\ der\ Waals} = \sum_i \sum_j \varepsilon(290000e^{-12.5/R} - 2.25R^{-6})$$

where

$$R = \frac{r_{ij}}{R_i^* + R_j^*}$$

The parameters include:

- **R_i^* and R_j^***: the van der Waals radii for the atoms
- **Epsilon (**ε): determines the depth of the attractive potential energy well and how easy it is to push atoms together
- **r_{ij}**: which is the actual distance between the atoms

At short distances the above equation favors repulsive over dispersive interactions. To compensate for this at short distances (R=3.311) this term is replaced with:

$$E_{vanderWalls} = 336.176 \sum_i \sum_j \varepsilon R^{-2}$$

The R* and Epsilon parameters are stored in the MM2 Atom Types table.
For certain interactions, values in the VDW interactions parameter table are used instead of those in the MM2 atom types table. These situations include interactions where one of the atoms is very electronegative relative to the other, such as in the case of a water molecule.

Cutoff parameters for van der Waals interactions

The use of cutoff distances for van der Waals terms greatly improves the computational speed for large molecules by eliminating long range, relatively insignificant, interactions from the computation.
ChemBio3D uses a fifth-order polynomial switching function so that the resulting force field maintains second-order continuity. The cutoff is implemented gradually, beginning at 90% of the specified cutoff distance. This distance is set in the MM2 Constants table.
The van der Waals interactions fall off as 1/r6, and can be cut off at much shorter distances, for example 10Å. This cut off speeds the computations significantly, even for relatively small molecules.

Note: *To precisely reproduce the energies obtained with Allinger's force field: set the van der Waals cutoff constants to large values in the MM2 Constants table.*

Electrostatic energy

The electrostatic energy is a function of the charge on the non-bonded atoms, *q*, their interatomic distance, *r*ij, and a molecular dielectric expression, *D*, that accounts for the attenuation of electrostatic interaction by the environment (solvent or the molecule itself).
In ChemBio3D, the electrostatic energy is modeled using atomic charges for charged molecules and bond dipoles for neutral molecules.
ChemBio3D accounts for these interactions:

- charge/charge
- dipole/dipole
- dipole/charge.

Each type of interaction uses a different form of the electrostatic equation:

$$E_{Electrostatic} = \sum_i \sum_j \frac{q_i q_j}{D r_{ij}}$$

charge/charge contribution

$$E = 332.05382 \sum_i \sum_j \frac{q_i q_j}{D_q r_{ij}}$$

where the value 332.05382 converts the result to units of kcal/mole.

dipole/dipole contribution

$$E = 14.388 \sum_i \sum_j \frac{\mu_i \mu_j}{D_\mu r_{ij}^3} (\cos\chi - 3\cos\alpha_i \cos\alpha_j)$$

where the value 14.388 converts the result from ergs/mole to kcal/mole, χ is the angle between the two dipoles μi and μj, αi and αj are the angles the dipoles form with the vector, rij, connecting the two at their midpoints, and Dm is the (effective) dielectric constant.

dipole/charge contribution

$$E = 69.120 \sum_i \sum_j \frac{q_i \mu_j}{r_{ij}^2 \sqrt{D_\mu D_q}} (\cos\alpha_j)$$

where the value 69.120 converts the result to units of kcal/mole.
Bond dipole parameters, μ, for each atom pair are stored in the bond stretching parameter table. The charge, *q*, is stored in the atom types table. The molecular dielectric expression is set to a constant value between 1.0 and 5.0 in the MM2 Atom types table.

📝 ***Note:*** *ChemBio3D does not use a distance-dependent dielectric.*

Cutoff parameters

The use of cutoff distances for electrostatic terms, as for van der Waals terms, greatly improves the computational speed for large molecules by eliminating long-range interactions from the computation.
As in the van der Waals calculations, ChemBio3D uses a fifth-order polynomial switching function to maintain second-order continuity in the force-field. The switching function is invoked as minimum values for charge/charge, charge/dipole, or dipole/dipole interactions are reached. These cutoff values are located in the MM2 Constants parameter table.
Since the charge-charge interaction energy between two point charges separated by a distance r is proportional to 1/r, the charge-charge cutoff must be rather large, typically 30 to 40Å, depending on the size of the molecule. The charge-dipole, dipole-dipole interactions fall off as $1/r^2$, $1/r^3$ and can be cutoff at much shorter distances, for example 25 and

18Å respectively. To precisely reproduce the energies obtained with Allinger's force field: set the cutoff constants to large values (99, for example) in the MM2 Constants table.

OOP bending

Atoms that are arranged in a trigonal planar fashion, as in sp2 hybridization, require an additional term to account for out-of-plane (OOP) bending. MM2 uses the following equation to describe OOP bending:

$$E = \sum_{Out\ of\ Plane} K_b[(\theta - \theta_o)^2 + SF(\theta - \theta_o)^6]$$

The form of the equation is the same as for angle bending, however, the θ value used is angle of deviation from coplanarity for an atom pair and θ is set to zero.
The special force constants for each atom pair are located in the Out of Plane bending parameters table. The sextic correction is used as previously described for Angle Bending. The sextic constant, SF, is located in the MM2 Constants table.

Pi bonds and atoms with pi bonds

For models containing pi systems, MM2 performs a Pariser-Parr-Pople pi orbital SCF computation for each system. A pi system is defined as a sequence of three or more atoms of types which appear in the Conjugate Pi system Atoms table. Because of this computation, MM2 may calculate bond orders other than 1, 1.5, 2, and so on.

Note: *The method used is that of D.H. Lo and M.A. Whitehead, Can. J. Chem., 46, 2027(1968), with heterocycle parameter according to G.D. Zeiss and M.A. Whitehead, J. Chem. Soc. (A), 1727 (1971). The SCF computation yields bond orders which are used to scale the bond stretching force constants, standard bond lengths and twofold torsional barriers.*

The basic process is:

1. A Fock matrix is generated based on the favorability of electron sharing between pairs of atoms in a pi system.
2. The pi molecular orbitals are computed from the Fock matrix.
3. The pi molecular orbitals are used to compute a new Fock matrix, then this new Fock matrix is used to compute better pi molecular orbitals.
4. Step 2 and 3 are repeated until the computation of the Fock matrix and the pi molecular orbitals converge. This method is called the self-consistent field technique or a pi-SCF calculation.
5. A pi bond order is computed from the pi molecular orbitals.
6. The pi bond order is used to modify the bond length(BLres) and force constant (Ksres) for each bond in the pi system.
7. The modified values of Ksres and BLres are used in the molecular mechanics portion of the MM2 computation to further refine the molecule.

Stretch-bend cross terms

Stretch-bend cross between bond stretching and angle bending. For example, when an angle is compressed, the MM2 force field uses the stretch-bend force constants to lengthen the bonds from the central atom in the angle to the other two atoms in the angle.

$$E = \sum_{Stretch/\ Bend} \frac{1}{2} K_{sb}(r - r_o)(\theta - \theta_o)$$

The force constant (Ksb) differs for different atom combinations.
The seven different atom combinations where force constants are available for describing the situation follow:

- X-B, C, N, O-Y
- B-B, C, N, O-H
- X-Al, S-Y
- X-Al, S-H
- X-Si, P-Y
- X-Si, P-H
- X-Ga, Ge, As, Se-Y, P-Y

where X and Y are any non-hydrogen atom.

User-imposed constraints

Additional terms are included in the force field when constraints are applied to torsional angles and non-bonded distances by the Optimal field in the measurement table. These terms use a harmonic potential function, where the force constant has been set to a large value (4 for torsional constraints and 106 for non-bonded distances) in order to enforce the constraint.
For torsional constraints the additional term and force constant is described by:

$$E = \sum_{Torsions} 4(\theta - \theta_o)^2$$

For non-bonded distance constraints the additional term and force constant is:

$$E = \sum_{Distance} 10^6 (r - r_o)^2$$

Molecular dynamics simulation

Molecular dynamics simulates molecular motion. This simulation is useful because motion is inherent to all chemical processes: vibrations, like bond stretching and angle bending, give rise to IR spectra; chemical reactions, hormone-receptor binding, and other complex processes are associated with many kinds of intramolecular and intermolecular motions.

It is a time dependent method to simulate the movement of atoms.
Conformational transitions and local vibrations are the usual subjects of molecular dynamics studies. Molecular dynamics alters the values of the intramolecular degrees of freedom in a stepwise fashion. The steps in a molecular dynamics simulation represent the changes in atom position over time, for a given amount of kinetic energy.
The Molecular Dynamics command in the **Calculations** menu can be used to compute a molecular dynamics trajectory for a molecule or fragment in ChemBio3D. A common use of molecular dynamics is to explore the conformational space accessible to a molecule, and to prepare sequences of frames representing a molecule in motion.
For more information on Molecular Dynamics, See "Computational Engines" on page 88.

Molecular dynamics formulas

The molecular dynamics computation consists of a series of steps that occur at a fixed interval, typically about 2.0 fs (femtoseconds, 1.0 x 10^{-15} seconds). The Beeman algorithm for integrating the equations of motion, with improved coefficients (B. R. Brooks) is used to compute new positions and velocities of each atom at each step.
Each atom (i) is moved according to the following formula:

$$x_i = x_i + v_i \Delta t + ((5a_i - a_i^{old})(\Delta t)^2)/8$$

Similarly, each atom is moved for y and z, where xi, yi, and zi are the Cartesian coordinates of the atom, v_i is the velocity, a_i is the acceleration, a_i^{old} is the acceleration in the previous step, and Δt is the time between the current step and the previous step. The potential energy and derivatives of potential energy (g_i) are then computed with respect to the new Cartesian coordinates.
New accelerations and velocities are computed at each step according to the following formulas (m_i is the mass of the atom):

Chemical properties

The ChemBioOffice 2012 suite lets you determine more than 100 different chemical, topological, physical, and thermodynamic properties. This guide describes the properties you can calculate using ChemBio3D and lists the property functions that are available in other ChemBioOffice 2012 applications.

ChemBio3D properties

The properties listed below can be calculated in ChemBio3D Ultra for ChemBioOffice 2012. For more information on a property and how to calculate it, click its link below.

B
Balaban Index
Boiling Point
C
Cp
Cv
Cluster Count
Connolly Accessible Area
Connolly Molecular Area
Connolly Solvent Excluded Volume
Critical Pressure
Critical Temperature
Critical Volume
D
Dipole
E
Electron Density
Electrostatic Potential
Elemental Analysis
Enthalpy
Entropy
Exact Mass
F
Formal Charge
Frequencies
G
Gibbs Free Energy
H
Harmonic Zero Point Energy
Heat Capacity
Heat of Formation
Henry's Law Constant
Hyper Polarizability
Hyperfine Coupling Constants
I
Ideal Gas Thermal Capacity
Internal Energy
Ionization Potential
K
Kinetic Energy
L
Lipinski Rule of five
LogP/Partition Coefficient
LogS
Lowdin Charges
Lowdin Populations
M
Mass
Melting Point
Mol Formula
Mol Formula HTML
Mol Refractivity
Mol Weight
Molecular Mass
Molecular Surfaces
Molecular Topological Index
Molecular Volume
Mulliken Charges
Mulliken Populations
m/z
N
Number of HBond Acceptors
Number of HBond Donors
Num Rotatable Bonds
O
Ovality
P
LogP/Partition Coefficient
pKa
Polar Surface Area
Polarizability
Potential Energy
Principal Moment
R
Radius
RMS Force
Num Rotatable Bonds
S
SCF Energy
Shape Attribute
Shape Coefficient
Spin Density
Sum Of Degrees
Sum of Valence Degrees
T
Thermodynamic Energy
Topological Diameter
Total Connectivity
Total Energy
Total Valence Connectivity
V
Vapor Pressure
W
Water Solubility
Wiener Index
Z
Zero-Point Energy

*For more information on the Molecular Networks properties, see "Additional computational engines" on page 1.

Balaban Index

The Balaban index, represented as J, is defined as:

$$J = \frac{q}{\mu + 1} \sum_{edges\,ij} (S_i S_j)^{-1/2}$$

Where:

- q is the number of edges in the molecular graph.
- μ= (q-n+1) is the cyclomatic number of molecular graph.
- n is the number of atoms in the molecular graph.
- S_i is the sum of all entries in the i^{th} row (or column) of the topological distance matrix of the molecule. The distance matrix stores the shortest path between all pairs of atoms.

To calculate the Balaban index:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Balaban Index**.
3. Click **OK**.

Boiling Point

The boiling point is report in Kelvin.

A solution boils at a slightly higher temperature than the pure solvent. The change in boiling point is calculated using the formula:

$$\Delta T_b = K_b m$$

Where K_b is the molal boiling point constant, m is the concentration of the solute expressed as molality, and ΔT_b is the change in temperature.

To report the boiling point:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Boiling Point**.
3. Click **OK**.

C_p

C_p is the heat capacity at constant pressure. It is defined as a differential quantity; the ratio of a small amount of heat, δQ, added to the body, to the corresponding small increase in its temperature, δT, as shown in formula:

$$C_p = \left(\frac{\delta Q}{dT}\right)_p = \left(\frac{\partial U + p\partial V}{\partial T}\right)_p$$

Where:

- C_p is the heat capacity at constant pressure.
- δQ is the small amount of heat added to the body.
- δT is the change in temperature.
- p is the pressure.
- U is the partial change in internal energy.
- V is the partial change in volume.
- T is the partial change in temperature.

To calculate C_p:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Cp**.
3. Click **OK**.

C_v

C_v is defined as the heat capacity at constant volume.
When heat, δQ, is introduced into the system, the change in its internal energy, δU is:

$\delta U = \delta Q - p\delta V$

If the process is performed at constant volume, the relation becomes:

$$\left(\frac{\delta Q}{dT}\right)_V = \left(\frac{\partial U}{\partial T}\right)_V = C_v$$

To calculate C_v:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Cv**.
3. Click **OK**.

Cluster Count

The cluster count is the number of paths of a given length in the distance matrix.
To calculate the cluster count:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Cluster Count**.
3. Click **OK**.

Connolly Accessible Area

This is the locus of the center of a spherical probe (representing the solvent) as it is rolled over the molecular model.
To report the Connolly accessible area:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Connolly Accessible Area**.
3. Click **OK**.

Connolly Molecular Area

This is the contact surface created when a spherical probe (representing the solvent) is rolled over the molecular model.
To report the Connolly molecular area:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Connolly Molecular Area**.
3. Click **OK**.

Connolly Solvent Excluded Volume

This is the volume of space bounded by the solvent accessible molecular surface.
To report the Connolly solvent excluded volume:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Connolly Solvent Excluded Volume**.
3. Click **OK**.

Critical Pressure

Reported in bars, this is the least applied pressure required at the critical temperature to liquefy a gas.
To report the boiling point:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Critical Pressure**.
3. Click **OK**.

Critical Temperature

Reported in Kelvin, this is the temperature above which a gas cannot be liquefied, regardless of the pressure applied.
To report the boiling point:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Critical Temperature**.

3. Click **OK**.

Critical Volume

Reported in cm^3/mol, this is the volume occupied by one mole of a substance at the critical temperature and pressure.
To report the boiling point:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Critical Volume**.
3. Click **OK**.

Dipole

Measured in Debye, the dipole refers to the separation of charge between two covalently bonded atoms. Dipoles can be characterized by their dipole moment, a vector quantity with a magnitude equal to the product of the charge or magnetic strength of one of the poles and the distance separating the two poles. Dipole moment is calculated using the formula:
μ=qr
Where μ is the dipole moment, q is the magnitude of the separated charge and r is a vector from the site of positive charge to the site of negative charge.
You can calculate the Dipole using either GAMESS or Gaussian.
To calculate the dipole using GAMESS:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Dipole** and click **Run**.
3. (Optional) To view the dipole in the model, select **Yes** when prompted.

To calculate the dipole using Gaussian:

4. Go to **Calculations**>**Gaussian Interface**>**Compute Properties**.
5. In the Gaussian interface dialog box, select the **Jobs** tab and then select the **Properties** tab.
6. In the Properties tab, select the **Dipole** checkbox.
7. Click **Run**.
8. (Optional) To view the dipole in the model, select **Yes** when prompted.

Electron Density

Is the probability of an electron being present at a specific location. It is calculated using the formula:

$$\rho(r) = \sum\sum P_{\mu\nu}\phi_{\mu}(r)\phi_{\nu}(r)$$

Where:

- $\rho(r)$, electron density, is a function of the coordinates r and is defined so that $\rho(r)dr$ is the number of electrons in a small volume, dr.
- $\phi_{\mu}(r)$ and $\phi_{\upsilon}(r)$ are basis functions.
- P is the density matrix.

You can calculate the electron density using either GAMESS or Gaussian.
To calculate electron density using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Electron Density**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface**>**Compute Properties.**
2. Select **Electron Density** and click **Run**.The results appear in the Atom Property window.

To calculate the electron density using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Electron Density**.
3. Click **OK**.

Another alternative method:

1. Go to **Calculations**>**Gaussian Interface**>**Compute Properties**.
2. In the Gaussian Interface dialog box, select the **Jobs** tab and then select the **Properties** tab.
3. In the Properties tab, select the **Electron Density** checkbox.
4. Click **Run**. The results appear in the Atom Property window.

Electrostatic Potential

The formula for electrostatic potential, V at a point, F for a system of charges, q_i is at points, r_i in a medium of dielectric constant ε is expressed as:

$$V = \sum_i \frac{q_i}{\varepsilon |r_i - F|}$$

You can calculate the electrostatic potential using GAMESS.
To calculate the electrostatic potential:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Electrostatic Potential**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Electrostatic Potential** and click **Run**.

Elemental Analysis

This is a process in which a material is analyzed for its elemental and isotopic composition. Elemental analysis can be qualitative (determining what elements are present) or quantitative (determining how much of each are present). To report perform an elemental analysis:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Elemental Analysis**.
3. Click **OK**.

Enthalpy

Enthalpy s a property of a substance that can be used to calculate the heat produced or absorbed in a chemical reaction. Enthalpy is also a state function; you can calculate the enthalpy change for a chemical reaction by finding the difference in enthalpy between the products and reactants. Enthalpy is calculated using the formula:

$H=U+PV$

Where:

- H is enthalpy
- U is internal energy
- P is pressure
- V is volume

To calculate enthalpy:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Enthalpy**.
3. Click **OK**.

Entropy

The change of entropy, dS is related to the amount of heat transfer, dQ and temperature, T by the formula:

$$dS = \frac{dQ}{T}$$

To calculate entropy using GAMESS:

1. Go to **Calculations**>**Compute Properties**.

2. Expand **GAMESS Interface** and select **Entropy**.
3. Click **OK**.

To calculate entropy using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Entropy**.
3. Click **OK**.

Exact Mass

This is the sum of the masses of the isotopes in a molecule. For example, the exact mass of water containing two hydrogen-1 (1H) and one oxygen-16 (16O) is 1.0078 + 1.0078 + 15.9994 = 18.0106. The exact mass of heavy water, containing two hydrogen-2 (deuterium or 2H) and one oxygen-16 (16O) is 2.014 + 2.014 + 15.9994 = 20.027.
To determine the exact mass:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Exact Mass**.
3. Click **OK**.

Formal Charge

The formal charge is the charge assigned to an atom in a molecule, assuming that electrons in a chemical bond are shared equally between atoms, regardless of relative electronegativity.
The formal charge of an atom in a molecule can be calculated using the formula:
FC=V-N-B/2
Where 'V' is the number of valence electrons of the atom in isolation (atom in ground state); 'N' is the number of non-bonding electrons on this atom in the molecule; and 'B' is the total number of electrons shared in covalent bonds with other atoms in the molecule.
To report the formal charge:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Formal Charge**.
3. Click **OK**.

Frequencies

To calculate infrared vibrational frequencies using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Frequencies**.
3. Click **OK**.

To calculate frequencies using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Frequencies**.
3. Click **OK**.

Gibbs Free Energy

Reported in KJ/mole, Gibbs free energy is defined as:

$$G(p, T) = U + pV - TS$$

which is same as:

$$G(p, T) = H - TS$$

Where:

- U is the internal energy (SI unit: Joule)
- p is pressure (SI unit: Pascal)
- V is volume (SI unit: m3)
- T is the temperature (SI unit: Kelvin)
- S is the entropy (SI unit: joule per Kelvin)
- H is the enthalpy (SI unit: Joule)

📝 ***Note:*** *H and S are thermodynamic values found at standard temperature and pressure.*

To calculate Gibbs free energy using either ChemPropPro or GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand either **GAMESS Interface** or **ChemPropPro** and select **Gibbs Free Energy**.
3. Click **OK**.

Harmonic Zero Point Energy

In ordinary quantum mechanics, the zero-point energy is the energy associated with the ground state of the system. One example is the energy associated with the ground state of the quantum harmonic oscillator, expressed by:

$$E = \frac{\bar{h}\omega}{2}$$

Where E is energy, $\bar{h}$ is reduced Planck constant, and ω is angular frequency.
To calculate frequencies using GAMESS:

1. Go to **Calculations**>**Compute Properties**.

2. Expand **GAMESS Interface** and select **Harmonic Zero Point Energy**.
3. Click **OK**.

Heat Capacity

The amount of heat required to change a substances temperature by a given amount. Values are measured in Cal/Mol-K.
To calculate heat capacity using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Heat Capacity**.
3. Click **OK**.

Heat of Formation

Reported in KJ/mole, the heat of formation is the increase in enthalpy resulting from the formation of one mole of a substance from its constituent elements at constant pressure.
To report the heat of formation:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Heat of Formation**.
3. Click **OK**.

Henry's Law Constant

A unitless value, Henry's Law Constant can be expressed as:

$$k_{H,pc} = \frac{p}{c}$$

Where 'p' is the partial pressure of the solute in the gas above the solution, 'c' is the concentration of the solute and '$k_{H,pc}$' is a constant with the dimensions of pressure divided by concentration. The constant, known as the Henry's law constant, depends on the solute, solvent, and temperature.
To report the heat of formation:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Henry's Law Constant**.
3. Click **OK**.

Hyper Polarizability

To calculate hyper polarizability using GAMESS:

1. Go to **Calculations**>**Compute Properties**.

2. Expand **GAMESS Interface** and select **Hyper Polarizability**.
3. Click **OK**.

Hyperfine Coupling Constants

To calculate hyperfine coupling constants using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Hyperfine Coupling Constants**.
3. Click **OK**.

Ideal Gas Thermal Capacity

The thermal capacity at constant volume of an ideal gas is:

$$C_V = \left(\frac{\delta U}{\delta T}\right)_V = \hat{c}_V Nk = \hat{c}_V nR$$

Where:

- c_V is a constant dependent on temperature
- U is the internal energy
- T is the absolute temperature
- V is the volume
- n is the amount of substance of the gas
- R is the gas constant (8.314 $JK^{-1}mol^{-1}$ in SI units)
- N is the number of gas particles
- k_B is the Boltzmann constant ($1.381\times10^{-23}JK^{-1}$ in SI units)

The thermal capacity at constant pressure of an ideal gas is:

$$C_p = \left(\frac{\delta H}{\delta T}\right)_p = (\hat{c}_V + 1)Nk$$

Where 'H' is the enthalpy of the gas, calculated as: H = U + pV.
To report the ideal gas thermal capacity:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Ideal Gas Thermal Capacity**.
3. Click **OK**.

Internal Energy

The internal energy is the total energy due to the motion of molecules, plus the rotation, and vibration of atoms within molecules. It can be calculated using:

$dU=TdS-PdV+\mu dN$

Where:

- dU is the change in internal energy
- T is the temperature
- dS is the change in disorder
- p is the pressure
- dV is the change in volume
- μ is the chemical potential
- dN is the number of particles added to the system

To calculate internal energy using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Internal Energy**.
3. Click **OK**.

Ionization Potential

The ionization potential is the energy needed to remove electrons from an atom.

To calculate ionization potential using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Ionization Potential**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **Ionization Potential** and click **Run.** The results appear in the Output window.

Kinetic Energy

The formula to calculate kinetic energy is:

$$K = p^2 / (2m)$$

Where K is the kinetic energy, m is the mass, and p is the momentum which is the product of mass and velocity, v.

To calculate kinetic energy using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Kinetic Energy**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface**>**Compute Properties.**
2. In the Properties tab, select **Kinetic Energy** and click **Run.**

Lipinski Rule of five

Reports the values necessary to determine the Lipinski rule of five:

- molecular weight
- number of HBond acceptors
- number of HBond donors
- number of rotatable bonds
- LogP

To report the Lipinski rule of five:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Lipinski Rule**.
3. Click **OK**.

Note: *You can also calculate the reported values separately.*

LogP/Partition Coefficient

The partition coefficient is a ratio of concentrations of un-ionized compound between two solutions. To measure the partition coefficient of ionizable solutes, the pH of the aqueous phase is adjusted so that the predominant form of the compound is un-ionized. The logarithm of the ratio of the concentrations of the un-ionized solute in the solvents is called LogP.
Normally, one of the solvents chosen is water; the second is hydrophobic, such as octanol.
The formula to calculate logP is:

$$\log P_{oct/wat} = \log\left(\frac{[solute]_{octanol}}{[solute]_{un-ionizedwater}}\right)$$

To calculate LogP:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Networks** and select **LogP**.

3. Click **OK**.

Alternative method #1:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **LogP**.
3. Click **OK**.

Alternative method #2:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ClogP Driver** and select **Partition Coefficient**.
3. Click **OK**.

LogS

The logarithm of the solubility of a substance, measured in mol/liter.
To calculate LogS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Networks** and select **LogS**.
3. Click **OK**.

Lowdin Charges

Is calculated using the formula:

$$q_k = Z_k - \sum_{i \in k} (S^{1/2} P S^{1/2})_{ii}$$

Where:

- Z_k is the nuclear charge
- P is the electronic density matrix
- $S^{1/2}$ is the square root of the overlap matrix
- Summation i runs over all basis functions centered on atom k.

To calculate Lowdin charges using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Lowdin Charges**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface**>**Compute Properties.**

2. In the Properties tab, select **Lowdin Charges** and click **Run.**

Lowdin Populations

In the Lowdin approach, the non-orthogonal atomic orbitals are transformed to an orthogonal set. The transformed orbitals, χ_b are given by:

$$\chi'_b = \sum_a (S^{-1/2})_{ab} \chi_a$$

In Lowdin Population Analysis (LPA), the α, β and gross electron populations associated with fragment A are:

$$GP_A^\alpha = \sum_{a \in A} (S^{1/2} P^\alpha S^{1/2})_{aa}$$

$$GP_A^\beta = \sum_{a \in A} (S^{1/2} P^\beta S^{1/2})_{aa}$$

$$GP_A = GP_A^\alpha + GP_A^\beta$$

The spin density is given by:

$$SP_A = GP_A^\alpha - GP_A^\beta$$

To calculate Lowdin population using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Lowdin Population**s.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface**>**Compute Properties.**
2. In the Properties tab, select **Lowdin Populations** and click **Run.**

Mass

This is the mass of one molecule of a substance, relative to the unified atomic mass unit u (equal to 1/12 the mass of one atom of 12C). Also called molecular mass.
To report the mass:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Mass**.
3. Click **OK**.

Melting Point

Is the temperature at which a solid becomes a liquid at standard atmospheric pressure. At the melting point, the solid and liquid phase exist in equilibrium. The formula to calculate melting point is:

$$T = \frac{\Delta H}{\Delta S}$$

Where 'T' is the temperature at the melting point, 'ΔS' is the change in entropy of melting, and 'ΔH' is the change in enthalpy of melting.

To report the melting point:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Melting Point**.
3. Click **OK**.

Mol Formula

This is the molecular formula of the compound.
To report the mass:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Molecular Formula**.
3. Click **OK**.

Mol Formula HTML

This is the molecular formula written in HTML format. You can copy and paste the output to an HTML file.
Here is an example of the output for a model of aniline:
C₆H₇N
To report the mol formula in HTML format:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Mol Formula HTML**.
3. Click **OK**.

Mol Refractivity

Is a measure of the total polarizability of one mole of a substance. It is dependent on the temperature, index of refraction, and pressure.
The molar refractivity, 'A' is expressed as:

$$A = \frac{4\pi}{3} N_A \alpha$$

Where 'N_A' is the Avogadro constant and α is the mean polarizability.
To report the Mol Refractivity using either ChemPropPro or ChemPropStd:

1. Go to **Calculations**>**Compute Properties**.
2. Expand either **ChemPropPro** or **ChemPropStd** and select **Mol Refractivity**.
3. Click **OK**.

Mol Weight

This is the sum of the atomic weights of all atoms in a molecule.
To report the mass:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Mol Weight**.
3. Click **OK**.

Molecular Mass

The mass of one molecule of a substance, measured in atomic units (au).

To calculate molecular mass using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Molecular Mass**.
3. Click **OK**.

Molecular Surfaces

To calculate molecular surfaces using GAMESS:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Molecular Surfaces** and click **Run.**

1. Go to **Calculations**>**Gaussian Interface**>**Compute Properties.**
2. In the Properties tab, select **Molecular Surfaces** and click **Run.**

Molecular Topological Index

Is a graph index defined by:

$$MTI = \sum_{i=1}^{n} E_i$$

Where E_i are the components of the vector:

$$E = (A + D)d$$

Where, A is the adjacency matrix and D is the graph distance matrix, and d is the vector of vertex degrees of a graph.

📝 ***Note:*** *An atom's degree is the number of non-hydrogen atoms to which it is adjacent.*

To calculate the molecular topological index:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Molecular Topological Index**.
3. Click **OK**.

Molecular Volume

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Molecular Volume**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **Molecular Volume** and click **Run.**

Mulliken Charges

The sum of GOP terms over all basis functions on a given atom A is called the Gross Atom Population or GAP_A. Mulliken charge for atom A is expressed as:

$$Q_A = Z_A - GAP_A$$

Where Z_A is the atomic number of atom A.
To calculate Mulliken charges using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Mulliken Charges**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Mulliken Charges** and click **Run.** The results appear in the Output window and the Atom Property table.

To calculate Mulliken charges using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Mulliken Charges**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **Mulliken Charges** and click **Run.** The results appear in the Output window and the Atom Property table.

Mulliken Populations

Mulliken Population Analysis (MPA) is a partitioning scheme based on the use of density and overlap matrices of allocating the electrons of a molecular entity in some fractional manner among its various parts (atoms, bonds, orbitals). MPA is arbitrary and strongly dependent on the particular basis set employed. However, comparison of population analyses for a series of molecules is useful for a quantitative description of intra-molecular interactions, chemical reactivity and structural regularities. According to MPA, the Gross Orbital Population (GOP) is:

$$GOP_{\mu} = \sum_{\nu} P_{\mu\nu}$$

P is population matrix, and is expressed for a closed shell as:

$$P_{\mu\nu} = (DS)_{\mu\nu}$$

S is the overlap matrix and D is density matrix. If the coefficients of the basis functions in the molecular orbital are $C_{\mu i}$ for the μ^{th} basis function in the i^{th} molecular orbital, the density matrix terms are expressed as:

$$D_{\mu\nu} = 2\sum_{i} C_{\mu i} C_{\nu i}$$

To calculate Mulliken populations using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Mulliken Charges**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Mulliken Populations** and click **Run.** The results appear in the Output window and the Atom Property table.

m/z

The mass-to-charge ratio is a physical quantity used in the electrodynamics of charged particles. Two particles with the same m/z ratio move in the same path in a vacuum when subjected to the same electric and magnetic fields.
To report the mass-to-charge ratio:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **m/z**.
3. Click **OK**.

Number of HBond Acceptors

The number of hydrogen bond acceptors in the model.
To report the value:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Number of HBond Acceptors**.
3. Click **OK**.

Number of HBond Donors

The number of hydrogen bond donors in the model.
To report the value:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Number of HBond Donors**.
3. Click **OK**.

Num Rotatable Bonds

The number of rotatable bonds in a molecule. A rotatable bond is defined as an acyclic bond drawn as a single bond (amide C-N bonds, O=C--N, are rotatable) where the atom on each end has at least one other non-hydrogen substituent. This topological parameter is a measure of molecular flexibility. Unsaturated bonds, and single bonds connected to hydrogens or terminal atoms, single bonds of amides, sulphonamides, and those connecting two hindered aromatic rings (having at least three ortho substituents) are considered non-rotatable.
To calculate the number of rotatable bonds:

1. Go to **Calculations**>**Compute Properties**.

2. Expand **Molecular Topology** and select **Num Rotatable Bonds**.
3. Click **OK**.

Ovality

This refers to a measure of how the shape of a molecule approaches a sphere (at one extreme) or a cigar shape (at the other). Ovality is described by a ratio of volume to area:

$$O = A / (4 \times \pi \times ((3 \times V) / 4 \times \pi)^{2/3})$$

Where 'A' is area, 'V' is Volume, and 'O' is Ovality.
The ovality of a helium atom is 1.0 and $HC_{24}H$ (12 triple bonds) is ~1.7 (equivalent to 1.7).
To report the ovality:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Ovality**.
3. Click **OK**.

pKa

The pKa describes the tendency of compounds or ions to dissociate in solution. If B is defined as the conjugate base of the acid HB, then pKa is calculated as:
pKa = -Log10(Ka)
where
Ka=[H+][B] / [HB]
To calculate pKa:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Networks** and select **pKa**.
3. Click **OK**.

Polar Surface Area

The Polar Surface Area (PSA) is defined as the surface sum over all polar atoms (usually oxygen and nitrogen) including attached hydrogens.
To calculate the PSA:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Polar Surface Area**.
3. Click **OK**.

Polarizability

The polarizability, α is defined as the ratio of the induced dipole moment of an atom to the electric field E that produces this dipole moment. The formula to calculate polarizability is:

$$\alpha = \frac{p}{E}$$

To calculate polarizability using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Polarizability**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Polarizability** and click **Run.**

To calculate polarizability using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **polarizability**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **polarizability** and click **Run.** The results appear in the Output window.

Potential Energy

Is an energy stored within a system. In a molecular system, potential energy is present in the chemical bonds in a molecule and also in forces between molecules.
To calculate potential energy using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Potential Energy**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Potential Energy** and click **Run.** The results appear in the Output window.

3. Click **Run**. The results appear in the Output window.

Principal Moment

This refers to the principal moments of inertia about the principal axes of a molecule. The moments of inertia are computed for a series of straight lines through the center of mass using the formula:

$$I = \sum_i m_i d_i^2$$

Where, 'I' is the moment of inertia, 'm_i's are point masses whose distances from the rotation axis are denoted by 'd_i's.

- Distances are established along each line proportional to the reciprocal of the square root of I on either side of the center of mass. The locus of these distances forms an ellipsoidal surface. The principal moments are associated with the principal axes of the ellipsoid.
- If all three moments are equal, the molecule is considered to be a symmetrical top. If no moments are equal, the molecule is considered to be an unsymmetrical top.

To report the principal moment:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropStd** and select **Principal Moment**.
3. Click **OK**.

Radius

The eccentricity of an atom is the largest value in its row (or column) of the distance matrix, and represents how far away from the molecular center it resides.

The diameter (D) is the maximum such value for all atoms, and is held by the most outlying atom(s). Examples: Diameter of methane = 0; ethane = 1; propane = 2; n-butane = 3.

The radius R is the minimum such value, and is held by the most central atom(s). Examples: Radius of methane = 0; ethane = 1; propane = 1; n-butane = 2.

To calculate the radius:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Radius**.
3. Click **OK**.

RMS Force

The root mean square force.

1. Go to **Calculations**>**Compute Properties**.

2. Expand **Gaussian Interface** and select **RMS Force**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **RMS Force** and click **Run.**

SCF Energy

The self-consistent field method for determining the ground state wave function of a quantum many-body system.

To calculate the SCF energy:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **SCF Energy**.
3. Click **OK**.

1. An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **SCF Energy** and click **Run.**

Shape Attribute

The shape attribute (kappa) measures the branching of a molecule, and is scaled so as to fall between the minimum and maximum values possible for the given order. The first-order shape attribute counts the number of one-bond paths. The second-order attribute counts the number of two-bond paths, and so on. The first three orders (1..3) are available.
To calculate the shape attribute:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Shape Attribute**.
3. Click **OK**.

Shape Coefficient

The shape coefficient, I is given by:

$$I = (D - R)/R$$

Where the diameter (D) is the maximum such value for all atoms, and is held by the most outlying atom(s). The radius (R) is the minimum such value, and is held by the most central atom(s).
Examples values for D: methane = 0; ethane = 1; propane = 2; n-butane = 3.

Example values for R: Radius: methane = 0; ethane = 1; propane = 1; n-butane = 2.

To calculate the shape coefficient:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Shape Coefficient**.
3. Click **OK**.

Spin Density

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Spin Density**.
3. Click **OK**.

1. An alternative method:

1. Go to **Calculations**>**Gaussian Interface>Compute Properties.**
2. In the Properties tab, select **Spin Density** and click **Run.**

Sum Of Degrees

Is the sum of degrees of every atom. An atom's degree is the number of nonhydrogen atoms to which it is bonded.
To calculate the sum of degrees:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Sum of Degrees**.
3. Click **OK**.

Sum of Valence Degrees

Is the sum of degrees of every atom. An atom's valence degree is equal to the sum of its adjacent bonds' orders, including hydrogens.
To calculate the sum of valence degrees:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Sum of Valence Degrees**.
3. Click **OK**.

Thermodynamic Energy

To calculate thermodynamic energy using Gaussian:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Thermodynamic Energy**.
3. Click **OK**.

Topological Diameter

Is the longest dimension of a molecule.

To calculate the topological diameter:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Topological Diameter**.
3. Click **OK**.

Total Connectivity

Is the connectivity considered over all the heteroatoms.

To calculate the total connectivity:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Total Connectivity**.
3. Click **OK**.

Total Energy

Is the sum of kinetic energy and potential energy.

To calculate total energy using GAMESS:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **GAMESS Interface** and select **Total Energy**.
3. Click **OK**.

An alternative method:

1. Go to **Calculations**>**GAMESS Interface>Compute Properties.**
2. In the Properties tab, select **Total Energy** and click **Run.** The results appear in the Output window.
3. Click **Run**. The results appear in the Output window.

Total Valence Connectivity

Is the valence connectivity considered over all the heteroatoms.

To calculate the total valence connectivity:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Total Valence Connectivity**.
3. Click **OK**.

Vapor Pressure

Is the pressure exerted by a vapor in equilibrium with its solid or liquid phase. Vapor pressure measures the concentration of solvent molecules in the gas phase.
Vapor pressure can be calculated using Raoult's law. The formula to calculate vapor pressure is:

$$p_{tot} = \sum_i p_i \chi_i$$

Where 'p' is vapor pressure, 'i' is a component index, and 'χ' is a mole fraction.
To report the vapor pressure:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Vapor Pressure**.
3. Click **OK**.

Water Solubility

Is the maximum amount of a substance that can be dissolved in water at equilibrium at a given temperature and pressure. Water solubility is measured in mg/L.
To report the water solubility:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **ChemPropPro** and select **Water Solubility**.
3. Click **OK**.

Wiener Index

Provides measure of branching defined as:

$$W = \frac{1}{2}\sum D_{ij}$$

Where D_{ij} are the off-diagonal elements of the distance matrix.
To calculate the Wiener Index:

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Molecular Topology** and select **Wiener Index**.
3. Click **OK**.

Zero-Point Energy

1. Go to **Calculations**>**Compute Properties**.
2. Expand **Gaussian Interface** and select **Zero-Point Energy**.
3. Click **OK**.

ChemBioFinder properties

The properties listed below can be calculated in ChemBioFinder Ultra for ChemBioOffice 2012. For more information on these properties and how to calculate them, see the ChemBioFinder online help.

B
Balaban Index
Boiling Point

C
Chemical Name
Cluster Count
Critical Pressure
Critical Temperature
Critical Volume
Connolly Accessible Area
Connolly Molecular Area
Connolly Solvent Excluded Volume

E
Elemental Analysis
Exact Mass

F
Formal Charge

G
Gibbs Free Energy

H
Heat of Formation
Henry's Law Constant

I
Ideal Gas Thermal Capacity

L
LogP
LogS

M
Mass
Melting Point
Mol Formula
Mol Formula HTML
Mol Refractivity
Mol Weight
Molecular Topological Index
m/z

N
Num Rotatable Bonds

O
Ovality

P
Partition Coefficient
pKa
Polar Surface Area
Principal Moment

R
Radius

S
Shape Attribute
Shape Coefficient
Sum of Degrees
Sum of Valence Degrees

T
Topological Diameter
Total Connectivity
Total Valence Connectivity

V
Vapor Pressure

W
Water Solubility
Wiener Index

ChemBioDraw properties

The properties listed below can be calculated in ChemBioDraw Ultra for ChemBioOffice 2012. For more information on these properties and how to calculate them, see the ChemBioDraw online help.

B
Boiling Point

H
Heat of Formation

P
pKa

C
Critical Pressure
Critical Temperature
Critical Volume
CLogP/CMR
G
Gibbs Free Energy
Henry's Law Constant
L
LogP
LogS
M
Melting Point
MR
T
tPSA

ChemDraw/Excel properties

The properties listed below can be calculated in ChemDraw/Excel for ChemBioOffice 2012. For more information on these properties and how to calculate them, see the ChemDraw/Excel online help.

B
Balaban index
Boiling point
C
Cluster count
Critical Pressure
Critical Temperature
Critical Volume
Connolly Molecular Surface Area
Connolly Solvent Accessible Surface Area
Connolly Solvent-Excluded Volume
G
Gibbs Free Energy
H
Heat of Formation
I
Ideal Gas Thermal Capacity
L
LogP
M
Molar Refractivity
N
Number of rotatable bonds
O
Ovality
P
Principal Moments of Inertia (X, Y, Z)
Polar Surface Area
R
Radius
S
Shape attribute
Shape coefficient
Sum of degrees
Sum of valence degrees
T
Total connectivity
Topological diameter
Topological index
Total valence connectivity
V
Vapor Pressure
W
Water Solubility
Wiener Index

Keyboard modifiers

The following tables list the keyboard modifiers that let you manipulate your view of the model without changing tools.

Rotation

Key	Drag	Shift+Drag
ALT	Select the Rotate tool and rotate all objects	Select the Rotate tool and rotate the selected object(s). At least one object must be selected.
SHIFT+B SHIFT+N		Rotate 1/2 of fragment around bond which fragment rotates depends on the order in which the atoms were selected.
V	Rotate all objects (at least one bond must be selected)	Rotate model about the axis. The model that includes the selected bond rotates around the bond.
X	Rotate all objects about X-axis	Rotate model about the X-axis
Y	Rotate all objects about Y-axis	Rotate model about the Y-axis
Z	Rotate all objects about Z-axis	Rotate model about the Z-axis

In addition to the keyboard shortcuts, you can rotate a model by dragging with the mouse while holding down both the middle mouse button or scroll wheel and the left mouse button.

Tip: *The order is important; press the middle button first.*

Zoom and translate

Key	Drag	Shift+Drag
CTRL	Move all objects	Move the selected model
A	Zoom to center	
Q	Zoom to rotation center	
W	Zoom to selection center	

If you have a wheel mouse, you can also use the scroll wheel to zoom. Dragging with the middle button or scroll wheel translates the view.

Selection

Standard selection

Hold down the S key to choose the selection tool. With the S key pressed, you can perform the actions shown in the table below:

Key	Click	SHIFT+click	Drag	SHIFT+drag
S	Select an atom or bond	Select multiple atoms or bonds as you click them	Select multiple atom or bonds in within a region	Multiple box select atom /bonds

Note: *Clicking a bond selects the bond and the two atoms connected to it. Double-clicking an atom or bond selects the fragment that atom or bond belongs to. Double-clicking a selected fragment selects the next higher fragment; that is, each double-click moves you up one in the hierarchy until you have selected the entire model.*

Radial selection

Radial selection is selection of an object or group of objects based on the distance or radius from a selected object or group of objects. This feature is useful for highlighting the binding site of a protein. Radial selection is accessed through the **Select** submenu of the context menu in the model explorer or 3D display.

In all cases, specify multiple selections by holding the SHIFT key down while making the selections.

Submenu option	Effect
Select Atoms within Distance of Selection	Selects all atoms (except for those already selected) lying within the specified distance from any part of the current selection. The current selection will be un-selected unless multiple selection is used.
Select Groups within Distance of Selection	Selects all groups (except for those already selected) that contain one or more atoms lying within the specified distance from any part of the current selection. The current selection will be un-selected unless multiple selection is used.
Select Atoms within Radius of Selection Centroid	Selects all atoms (except for those already selected) lying within the specified distance of the centroid of the current selection. The current selection will be un-selected unless multiple selection is used.
Select Groups within Radius of Selection Centroid	Selects all groups (except for those already selected) that contain one or more atoms lying within the specified distance of the centroid of the current selection. The current selection will be un-selected unless multiple selection is used.

2D to 3D Conversion

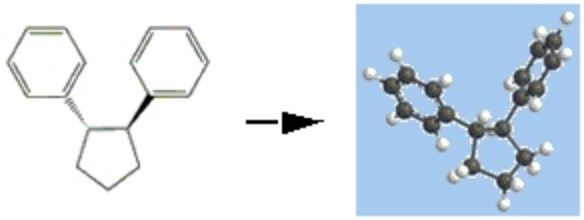
This section describes how ChemBio3D performs the conversion from two to three dimensions. You can open a 2D drawing using several methods.

- Opening a ChemBioDraw or ISIS/Draw document.
- Pasting a ChemBioDraw or ISIS/Draw structure from the Clipboard.
- Opening a ChemBioDraw connection table file.

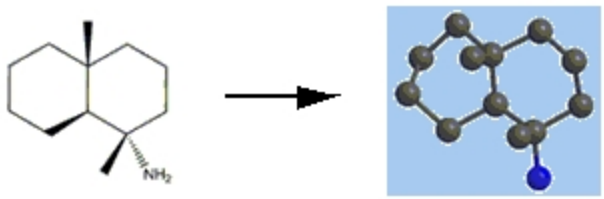
While ChemBio3D can read and assimilate any ChemBioDraw structure, you can assist ChemBio3D in the two- to three-dimensional conversion of your models by following the suggestions in this chapter.
ChemBio3D uses the atom labels and bonds drawn in ChemDraw to form the structure of your model. For every bond drawn in ChemDraw, a corresponding bond is created in ChemBio3D. Every atom label is converted into at least one atom.
Dative bonds are converted to single bonds with a positive formal charge added to one atom (the atom at the tail of the dative bond) and a negative formal charge added to the other (the head of the dative bond).

Stereochemical relationships

ChemBio3D uses the stereo bonds H-Dot, and H-Dash atom labels in a ChemBioDraw structure to define the stereochemical relationships in a model. Wedged bonds in ChemBioDraw 13.0 indicate a bond where the atom at the wide end of the bond is in front of the atom at the narrow end of the bond. Wedged hashed bonds indicate the opposite: the atom at the wide end of a wedged hashed bond is behind the atom at the other end of the bond.

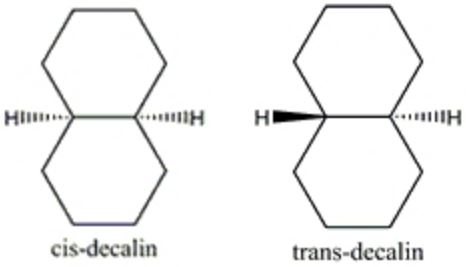


As shown above, the two phenyl rings are a *trans* formation about the cyclopentane ring. The phenyl ring on the left is attached by a wedged hashed bond; the phenyl ring on the right is attached by a wedged bond.
You can also use dashed, hashed, and bold bonds. However, be aware of potential ambiguity where these non-directional bonds are used. A dashed, hashed, or bold bond must be between one atom that has at least three attachments and one atom that has no more than two attachments, including the dashed, hashed, or bold bond. Shown below, the nitrogen atom is placed behind the ring system and the two methyl groups are placed in front of the ring system. Each of these three atoms is bonded to only one other atom, so they are presumed to be at the wide ends of the stereo bonds.



However, in the next figure (below), the hashed bond is ambiguous because both atoms on the hashed bond are attached to more than two bonds. In this case the hashed bond is treated like a solid bond. Wavy bonds are always treated like solid bonds.

H-Dots and H-Dashes are also used to indicate stereochemistry. H-Dots become hydrogen atoms attached to carbon atoms by a wedged bond. H-Dashes become hydrogen atoms attached by a wedged hashed bond.
The following figure shows cis-decalin on the left and trans-decalin on the right as they would be drawn in Chem-BioDraw to be read in by ChemBio3D. Of course, you can specify a cis fusion with two H-Dots instead of two H-Dashes
.



As a general rule, the more stereo bonds you include in your model, the greater is the probability that ChemBio3D 13.0 will make correct choices for chirality and dihedral angles.
When converting two-dimensional structures, ChemBio3D 13.0 uses standard bond lengths and angles as specified in the current set of parameters. If ChemBio3D 13.0 tries to translate strained ring systems, the ring closures will not be of the correct length or angle.

Labels

ChemBio3D 13.0 uses the atom labels in a two-dimensional structure to determine the atom types of the atoms. Unlabeled atoms are assumed to be carbon. Labels are converted into atoms and bonds using the same method as that used to convert the text in a text box into atoms and bonds. Therefore, labels can contain several atoms or even substructures.

File Formats

Editing file format atom types

Some file formats contain information that describes the atom types. Typically, these atom types are ordered by some set of numbers, similar to the atom type numbers used in the Atom Types table. If the file format needs to support additional types of atoms, you can supply those types by editing the file format atom types.

ChemBio3D 13.0 uses XML tables to store file formats. You can edit these tables in any text editor or in ChemBio3D. Go to **View**>**Parameter Tables**) and select the table you want to edit.

Tip: *The XML files are in the path ...\Chem3D\C3D Items*

Name

Each atom type is described by a name. This name is a number found in files of the format described by the file format. All names must be unique. The records in the table window are sorted by name.

Note: *While names are similar to atom type numbers, they do not have to correspond to the atom type numbers of atom types. In some cases, however, they do correspond.*

Description

The second field contains a description of the atom type, such as C Alkane. This description is included for your reference only.

The remaining fields contain information corresponding to the information in an Atom Types table.

Native formats

There are three file formats that are native to ChemBio3D. Unless you plan to use a model in another application, you will want to save it in one of the native formats.

Chem3D XM. Compatible with ChemBio3D version 9.0 or later.

Chem3D 8.0. Compatible with Chem3D versions 4.0 to 8.0.

Chem3D 3.2. Compatible with Chem3D version 3.2 or earlier.

File format examples

The following sections provide examples of the files created when you save ChemBio3D files using the provided file formats.

Alchemy file

The sample Alchemy file (Alchemy) below was created using ChemBio3D for a model of cyclohexanol. The numbers in the first column are line numbers that are added for reference only.

```
 1 19 ATOMS 19 BONDS
 2     1 C3  -1.1236  -0.177   0.059
 3     2 C3    -0.26  -0.856 -1.0224
 4     3 C3     1.01 -0.0491 -1.3267
 5     4 C3    1.838  0.1626 -0.0526
 6     5 C3   0.9934  0.8543  1.0252
 7     6 C3  -0.2815  0.0527  1.3275
 8     7 O3  -2.1621 -1.0585  0.3907
 9      8 H  -1.4448  0.8185 -0.3338
10      9 H  -0.8497  -0.979 -1.9623
11     10 H   0.0275 -1.8784 -0.6806
12     11 H   1.6239 -0.5794 -2.0941
13     12 H    0.729  0.9408 -1.7589
14     13 H    2.197 -0.8229  0.3289
15     14 H   2.7422  0.7763  -0.282
16     15 H   1.5961  0.9769  1.9574
17     16 H   0.7156  1.8784   0.679
18     17 H  -0.8718  0.6068  2.0941
19     18 H   -0.004 -0.9319  1.7721
20     19 H  -2.7422  -0.593  0.9688
21        1        1       2  SINGLE
22        2        1       6  SINGLE
23        3        1       7  SINGLE
24        4        1       8  SINGLE
25        5        2       3  SINGLE
26        6        2       9  SINGLE
27        7        2      10  SINGLE
28        8        3       4  SINGLE
29        9        3      11  SINGLE
30       10        3      12  SINGLE
31       11        4       5  SINGLE
32       12        4      13  SINGLE
```

```
33      13       4      14  SINGLE
34      14       5       6  SINGLE
35      15       5      15  SINGLE
36      16       5      16  SINGLE
37      17       6      17  SINGLE
38      18       6      18  SINGLE
40      19       7      19  SINGLE
```

Alchemy file format

📝 ***Note:*** *Alchemy III is a registered trademark of Tripos Associates, Inc.*

Each line represents a data record containing one or more fields of information about the molecule. The fields that ChemBio3D uses are:

- Line 1 contains two fields. The first field is the total number of atoms in the molecule and the second field is the total number of bonds.
- Lines 2–20 each contain five fields of information about each atom in the molecule. The first field is the serial number of the atom; the second field is the atom type; the remaining fields are the X-, Y-, and Z- coordinates.

📝 ***Note:*** *You can modify and create atom types in the Alchemy file format. See "Editing file format atom types" on page 250 for instructions.*

- Lines 21–40 describe the bonds in the molecule. The first field is the bond number (ranging from 1 to the number of bonds), the second field is the serial number of the atom where the bond begins, the third field is the serial number of the atom where the bond ends, and the fourth field is the bond type. The possible bond types are: SINGLE, DOUBLE, TRIPLE, AMIDE, or AROMATIC. Note that all the bond order names are padded on the right with spaces to eight characters.

FORTRAN. The FORTRAN format for each record of the Alchemy file is as follows :

Line Number	Description	FORTRAN Format
1	number of atoms, number of bonds	I5, 1X, ATOMS,1X,I5,1X, BONDS
2–20	atom serial number, type, and coordinates	I6,A4,3(F9.4)
21–40	bond id, from atom, to atom, bond type	I6,I5,I6,2X,A8

Cartesian coordinate files

ChemBio3D lets you save models in Cart Coords 1 or Cart Coords 2 file formats. These file formats store the atom types, coordinates, and attached atoms for each atom in a model. These file formats also interpret fractional cell coordinates in orthogonal or non-orthogonal coordinate systems.

The difference between the two file formats are the codes used to convert atom type numbers in the file into atom types that ChemBio3D uses. In Cart Coords 1, atom types are numbered according to the numbering used by N.L. Allinger in MM2. These numbers are also generally followed by the program PC Model. In Cart Coords 2, the atom type number for all atom types is computed by multiplying the atomic number of the element by 10 and adding the number of valences as specified by the geometry of the atom type. These numbers are also generally followed by the program MacroModel.

For example, the atom type number for C Alkane (a tetrahedral carbon atom) is 64 using Cart Coords 2.

To examine the atom types described by a file format, see "Editing file format atom types" on page 250.

The format for a Cartesian coordinate file is:

```
19
 C   1      0.7066     1.0661      0.5088  1   2   4  9 10
 C   2     -0.8347     1.0755      0.5087  1   1   3 10 11
 C   3     -1.4090     0.2755     -0.6689  1   2   6 12 13
 C   4      1.2172    -0.3863      0.5088  1   1   5 14 15
 C   5      0.6393    -1.1915     -0.6644  1   4   6 16 17
 C   6     -0.8944    -1.1698     -0.6466  1   3   5 18 19
 O 101      1.1929     1.8096      1.5934  6   1 102
 H   9      1.0525     1.5595     -0.4322  5   1
 H  10     -1.2116     2.1250      0.4570  5   3
 H  11     -1.2089     0.6405      1.4656  5   3
 H  12     -2.5249     0.2816     -0.6258  5   4
 H  13     -1.1155     0.7623     -1.6294  5   4
 H  14      0.9370    -0.8781      1.4700  5   5
 H  15      2.3297    -0.4102      0.4377  5   5
 H  16      1.0034    -2.2463     -0.6182  5   6
 H  17      1.0057    -0.7613      -1.627  5   6
 H  18     -1.2950    -1.7316     -1.5245  5   7
 H  19     -1.2651    -1.6852      0.2712  5   7
 H 102      2.1275     1.8656      1.4899 21 101
```

Figure 14.1: A Cart Coords 1 table for cyclohexanol.

1. The first line of data contains the number of atoms in the model.

Optionally, you can follow the number of atoms in the file with crystal cell parameters for the crystal structure: a, b, c, α, β, and γ. Following the cell parameters, you can also include an exponent. If you include an exponent, then all of the fractional cell coordinates will be divided by 10 raised to the power of the exponent.

2. The first line of a Cartesian coordinate file is followed by one line of data for each atom in the model. Each line describing an atom begins with the symbol for the atom. This symbol corresponds to a symbol in the Elements table. The symbol can include a charge, such as N+. The symbol is followed by the serial number.
3. The serial number is followed by the three coordinates of the atom. If you have specified crystal cell parameters in the first line of the file, then these numbers are the fractional cell coordinates. Otherwise, the three numbers are X, Y, and Z Cartesian coordinates.
4. Following the coordinates is the atom type number of the atom type for this atom. This number corresponds to the code of an atom type record specified in the file format atom type table. For more information, see "Editing file format atom types" on page 250.
5. Following the atom type number is the connection table for the atom. You can specify up to ten other atoms. The connection table for a Cartesian coordinate file can be listed in one of two ways: by serial number or by position.

Connection tables by serial number use the serial number of each atom to determine the number that appears in the connection table of other atoms. All serial numbers must, therefore, be unique.
Connection tables by position use the relative positions of the atoms in the file to determine the number for each atom that will appear in the connection table of other atoms. The first atom is number 1, the second is 2, etc.

6. To create multiple views of the same set of atoms, you can flow the descriptions of the atoms with an equal number of lines corresponding to the same atoms with different coordinates. ChemBio3D generates independent views using the additional sets of coordinates.

Cambridge Crystal Data Bank files

You can import Cambridge Crystal Data Bank (CCDB) files but not save files in the CCDB format. ChemBio3D uses the FDAT format of CCDB, described on pages 26–42 of the data file specifications of the Cambridge Structural Database, Version 1 File Specifications from the Cambridge Crystallographic Data Centre. For further details about the FDAT format, refer to the above publication or contact the Cambridge Crystallographic Data Centre.
As described in the specifications of the Cambridge Crystal Data Bank format, bonds are automatically added between pairs of atoms whose distance is less than that of the sum of the covalent radii of the two atoms. The bond orders are guessed based on the ratio of the actual distance to the sum of the covalent radii. The bond orders, bond angles, and the atom symbols are used to determine the atom types of the atoms in the model.

Bond Type	Actual Distance / Sum of Covalent Radii
Triple	0.81
Double	0.87
Delocalized	0.93
Single	1.00

Internal coordinates file

Internal coordinates files (INT Coords) are text files that describe a single molecule by the internal coordinates used to position each atom. The serial numbers are determined by the order of the atoms in the file. The first atom has a serial number of 1, the second is number 2, etc.
The format for Internal coordinates files is as follows:

1. Line 1 is a comment line. ChemBio3D ignores this line. Each subsequent line begins with the building type number.
2. Line 2 contains the building type number of the Origin atom.
3. Beginning with line 3, the building type number is followed by the serial number of the atom to which the new atom is bonded and the distance to that atom. The origin atom is always the first distance-defining atom in the file. All distances are measured in Angstroms.
4. Beginning with line 4, the distance is followed by the serial number of the first angle-defining atom and the angle between the newly defined atom, the distance-defining atom, and the first angle-defining atom. All angles are measured in degrees.
5. Beginning with line 5, the serial number of a second angle-defining atom and a second defining angle follows the first angle. Finally, a number is given that indicates the type of the second angle. If the second angle type is zero, the second angle is a dihedral angle: New Atom – Distance-defining Atom – First Angle-defining Atom – Second Angle-defining Atom. Otherwise the third angle is a bond angle: New Atom – Distance-defining Atom – Second Angle-defining Atom. If the second angle type is 1, then the new atom is defined using a Pro-R/Pro-S relationship to the three defining atoms; if the second angle type is -1, the relationship is Pro-S.

Note: *You cannot position an atom in terms of a later-positioned atom.*

The following is a sample of an Internal coordinates output file for cyclohexanol, created in ChemBio3D:

```
1

1 1 1.54146

1 2 1.53525 1 111.7729

1 1 1.53967 2 109.7132 3  -55.6959  0
```

```
 1 4 1.53592 1  111.703 2   55.3112  0
 1 3 1.53415 2 110.7535 1   57.0318  0
 6 1 1.40195 2 107.6989 3 -172.6532  0
 5 1 1.11742 2   109.39 4    109.39 -1
 5 2 1.11629 1   109.41 3    109.41  1
 5 2 1.11568 1   109.41 3    109.41 -1
 5 3 1.11664 2   109.41 6    109.41 -1
 5 3 1.11606 2   109.41 6    109.41  1
 5 4 1.11542 1   109.41 5    109.41  1
 5 4 1.11493 1   109.41 5    109.41 -1
 5 5 1.11664 4   109.41 6    109.41  1
 5 5 1.11617 4   109.41 6    109.41 -1
 5 6 1.11664 3   109.41 5    109.41  1
 5 6 1.11606 3   109.41 5    109.41 -1
21 7   0.942 1 106.8998 2    59.999  0
 5 6
```

Bonds. Bonds are indicated in Internal coordinates files in two ways.

First, a bond is automatically created between each atom (except the Origin atom) and its distance-defining atom.

Second, if there are any rings in the model, ring-closing bonds are listed at the end of the file. If there are ring-closing bonds in the model, a blank line is included after the last atom definition. For each ring-closure, the serial numbers of the two atoms which comprise the ring-closing bond are listed on one line. The serial number of the first atom is 1, the second is 2, etc. In the prior Internal coordinates output example of cyclohexanol, the numbers 5 and 6 are on a line at the end of the file, and therefore the ring closure is between the fifth atom and the sixth atom.

If a bond listed at the end of an Internal coordinates format file already exists (because one of the atoms on the bond is used to position the other atom on the bond) the bond is removed from the model. This is useful if you want to describe multiple fragments in an internal coordinates file.

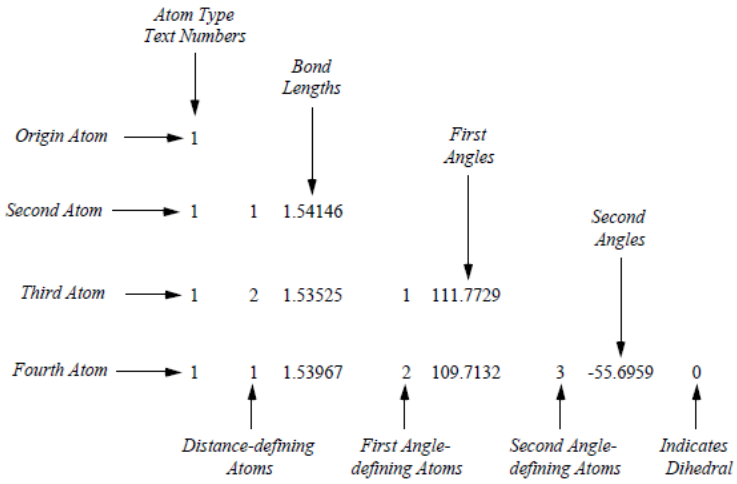


Figure 14.2: Components of an Internal coordinates File for C(1) through C(4) of Cyclohexanol.

In this illustration, the origin atom is C(1). C(2) is connected to C(1), the origin and distance defining atom, by a bond of length 1.54146 Å. C(3) is connected to C(2) with a bond of length 1.53525 Å, and at a bond angle of 111.7729 degrees with C(1), defined by C(3)-C(2)-C(1). C(4) is attached to C(1) with a bond of length 1.53967 Å, and at a bond angle of 109.7132 degrees with C(2), defined by C(4)-C(1)-C(2). C(4) also forms a dihedral angle of -55.6959 degrees with C(3), defined by C(4)-C(1)-C(2)-C(3).

This portion of the Internal coordinates file for C(1) through C(4) of Cyclohexanol can be represented by the following structural diagram:

FORTRAN formats. The FORTRAN formats for the records in an Internal coordinates file are as follows:

Line Number	Description	FORTRAN Format
Comment	Ignored	
Origin Atom		I4
Second Atom		I4, 1X, I3, 1X, F9.5
Third Atom		I4, 2(1X, I3, 1X, F9.5)
Fourth Atom to Last Atom		I4, 3(1X, I3, 1X, F9.5), I4

Blank Line		
Ring Closure Atoms		2(1X, I4)

MacroModel

MacroModel is produced within the Department of Chemistry at Columbia University, New York, N.Y. The MacroModel file format is defined in the “MacroModel Structure Files” version 2.0 documentation. The following is a sample file that describes a model of cyclohexanol.

```
19   cyclohexanol
 3   2   1   6   1  7 1 18 1 0 0 0 0 -1.396 0.3501 1.055 0
 3   1   1   3   1  8 1  9 1 0 0 0 0 -0.455 -0.740 1.587 0
 3   2   1   4   1 10 1 11 1 0 0 0 0  0.511 -1.222 0.497 0
 3   3   1   5   1 12 1 13 1 0 0 0 0  1.302 -0.048 -0.10 0
 3   4   1   6   1 14 1 15 1 0 0 0 0  0.372 1.0566 -0.62 0
 3   1   1   5   1 16 1 17 1 0 0 0 0 -0.606 1.5251 0.459 0
41   1   1   0   0  0 0  0 0 0 0 0 0 -2.068 -0.083 0.277 0
41   2   1   0   0  0 0  0 0 0 0 0 0 -1.053 -1.603 1.968 0
41   2   1   0   0  0 0  0 0 0 0 0 0  0.127 -0.340 2.451 0
41   3   1   0   0  0 0  0 0 0 0 0 0  1.222 -1.972 0.925 0
41   3   1   0   0  0 0  0 0 0 0 0 0 -0.058 -1.742 -0.30 0
41   4   1   0   0  0 0  0 0 0 0 0 0  1.972 0.3806 0.679 0
41   4   1   0   0  0 0  0 0 0 0 0 0  1.960 -0.413 -0.92 0
41   5   1   0   0  0 0  0 0 0 0 0 0  0.981 1.9214 -0.99 0
41   6   1   0   0  0 0  0 0 0 0 0 0 -1.309 2.2832 0.037 0
41   6   1   0   0  0 0  0 0 0 0 0 0 -0.033 2.0317 1.272 0
41   1   1   0   0  0 0  0 0 0 0 0 0 -2.052 0.7172 1.881 0
42  15   1   0   0  0 0  0 0 0 0 0 0  0.275 0.3749 -2.41 0
```

Each line represents a data record containing one or more fields of information about the model. Each field is delimited by space(s) or a tab. Line 1 contains two fields. The first field is the number of atoms in the model; the second field is the name of the molecule. The molecule name is the file name when the file is created using ChemBio3D.

1. Lines 2-19 each contain 17 fields describing information about one atom and its attached bond:

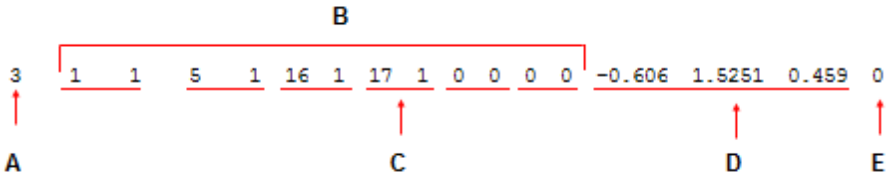


Figure 14.3: In the MacroModel file format, each row describes the location and attachments for an atom. A) The atom type for the atom; B) The atom pairs for the atoms that are bonded; C) The first number of each atom pair is the serial number for the bonded atom, the second number is the bond type used; D) The X- Y-, and Z-coordinates of the atom; E) the atom color.

Note: *ChemBio3D ignores atom colors. This color field will contain a zero if the file was created using ChemBio3D.*

Note: *Atom types are user-definable. See "Editing file format atom types" on page 250 for instructions on modifying or creating an atom type.*

FORTRAN Formats. The FORTRAN format for each record of the MacroModel format is as follows:

Line Number	Description	FORTRAN Format
1	number of atoms and molecule name (file name	1X,I5,2X,A

MDL MolFile

The MDL MolFile format is defined in the article “Description of Several Chemical Structure File Formats Used by Computer Programs Developed at Molecular Design Limited found in the Journal of Chemical Information and Computer Science, Volume 32, Number 3, 1992, pages 244–255.

Note: *MDL MACCS-II is a product of MDL Information Systems, Inc. (previously called Molecular Design, Limited).*

The following is a sample MDL MolFile file created using Chem3D Pro. This file describes a model of cyclohexanol (the line numbers are added for reference only):

```
1          cyclohexanol
2
3
```

```
 4          19          19           0 0 0
 5     -1.3488      0.1946      1.0316 C 0 0 0 0 0
 6     -0.4072     -0.8965      1.5632 C 0 0 0 0 0
 7      0.5621     -1.3777      0.4733 C 0 0 0 0 0
 8      1.3507     -0.2045     -0.1277 C 0 0 0 0 0
 9      0.4203      0.9011     -0.6518 C 0 0 0 0 0
10      -0.559      1.3696      0.4359 C 0 0 0 0 0
11     -0.3007      0.4266     -1.7567 O 0 0 0 0 0
12     -2.0207      -0.239       0.253 H 0 0 0 0 0
13     -2.0051      0.5617      1.8571 H 0 0 0 0 0
14     -1.0054     -1.7589      1.9444 H 0 0 0 0 0
15      0.1749     -0.4961      2.4273 H 0 0 0 0 0
16        1.27     -2.1277      0.9014 H 0 0 0 0 0
17     -0.0103     -1.8981     -0.3309 H 0 0 0 0 0
18      2.0207       0.225      0.6551 H 0 0 0 0 0
19      2.0084     -0.5688     -0.9529 H 0 0 0 0 0
20      1.0296        7659     -1.0161 H 0 0 0 0 0
21     -1.2615      2.1277      0.0139 H 0 0 0 0 0
22      0.0143      1.8761      1.2488 H 0 0 0 0 0
23      0.3286      0.2227     -2.4273 H 0 0 0 0 0
24           1           2           1 0 0 0
25           1           6           1 0 0 0
26           1           8           1 6 0 0
27           1           9           1 1 0 0
28           2           3           1 6 0 0
29           2          10           1 0 0 0
30           2          11           1 1 0 0
31           3           4           1 0 0 0
32           3          12           1 0 0 0
33           3          13           1 6 0 0
34           4           5           1 0 0 0
35           4          14           1 1 0 0
```

```
36          4          15          1 6 0 0
37          5           6          1 1 0 0
38          5           7          1 6 0 0
39          5          16          1 0 0 0
40          6          17          1 0 0 0
41          6          18          1 1 0 0
42          7          19          1 6 0 0
```

Each line represents either a blank line, or a data record containing one or more fields of information about the structure. Each field is delimited by a space(s) or a tab.

The fields in the MDL MolFile format used by Chem3D Pro are described below:

1. Line 1 starts the header block, which contains the name of the molecule. The molecule name is the file name when the file was created using Chem3D Pro.
2. Line 2 continues the Header block, and is a blank line.
3. Line 3 continues the Header block, and is another blank line.
4. Line 4 (the Counts line) contains 5 fields which describes the molecule: The first field is the number of atoms, the second field is the number of bonds, the third field is the number of atom lists, the fourth field is an unused field and the fifth field is the stereochemistry.

Note: *Chem3D Pro ignores the following fields: number of atom lists, the unused field and stereochemistry. These fields will always contain a zero if the file was created using Chem3D Pro.*

5. Lines 5–23 (the Atom block) each contain 9 fields which describes an atom in the molecule: The first field is the X coordinate, the second field is the Y coordinate, the third field is the Z coordinate, the fourth field is the atomic symbol, the fifth field is the mass difference, the sixth field is the charge, the seventh field is the stereo parity designator, the eighth field is the number of hydrogens and the ninth field is the center.

Note: *Chem3D Pro ignores the following fields: mass difference, charge, stereo parity designator, number of hydrogens, and center. These fields contain zeros if the file was created using Chem3D Pro.*

6. Lines 24–42 (the Bond block) each contain 6 fields which describe a bond in the molecule: the first field is the from-atom id, the second field is the to-atom id, the third field is the bond type, the fourth field is the bond stereo designator, the fifth field is an unused field and the sixth field is the topology code.

Note: *Chem3D Pro ignores the unused field and topology code. These fields will contain zeros if the file was created using Chem3D Pro.*

Limitations. The MDL MolFile format does not support non-integral charges in the same way as Chem3D Pro. For example, in a typical MDL MolFile format file, the two oxygens in a nitro functional group (NO_2) contain different charges: -1 and 0. In ChemBio3D models, the oxygen atoms each contain a charge of -0.500.

FORTRAN formats. The FORTRAN format for each record of the MDL MolFile format is as follows:

Line Number	Description	FORTRAN Format
1	Molecule name (file name)	A
2	Blank line	
3	Blank line	
4	Number of atoms Number of bonds	5I3
5–23	Atom coordinates, atomic symbol	3F10.4,1X,A2,5I3
24–42	Bond id, from atom, to atom, and bond type	6(1X,I2)

MSI MolFile

The MSI MolFile is defined in Chapter 4, “Chem-Note File Format” in the Centrum: Chem-Note™ Application documentation, pages 4-1 to 4-5. The following is a sample MSI MolFile file created using Chem3D Pro for cyclohexanol (the line numbers are added for purposes of discussion only):

: MSI Molfile format

```
 1              ! Polygen 133
 2                                Polygen Corporation: ChemNote molecule file (2D)
 3                                                     * File format version number
 4                                             90.0928
 5                                  * File update version number
 6                                   92.0114
 7                                 * molecule name
 8                                      cyclohexanol-MSI
 9                               empirical formula
10                                    Undefined Empirical Formula
11                                          * need 3D conversion?
12                                                   0
13                                * 3D displacement vector
```

```
14                                        0.000 0.000 0.000
15                          * 3D rotation matrix
16                          1.000 0.000 0.000 0.000 1.000 0.000 0.000 0.000 1.000
17                                                * 3D scale factor
18                         0
19                                    * 2D scale factor
20                         1
21                                * 2D attributes
22                        1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
23                                * 3D attributes
24                                       0 0 0 0 0 0 0 0 0 0 0
25                          * Global display attributes
26                                    1 0 1 12 256
27                               * Atom List
28                                     * Atom# Lbl Type x y x y z bits chrg ichrg frag istp lp chrl ring frad name seg grp FLAGS
29                        1      C      10      0      0      -1   0.46      0.2    0      0  0 0 0 0 0 0 0 0 C 1 0 -1 0 0 0 0 0 0 [C]
30                         2      C      10      0      0      1.2   -1.1      0.2    0      0  0 0 0 0 0 0 0 0 C 2 0 -1 0 0 0 0 0 0 [C]
30                         2      C      10      0      0      1.2   -1.1      0.2    0      0  0 0 0 0 0 0 0 0 C 2 0 -1 0 0 0 0 0 0 [C]
31                         3      C      10      0      0      0.1   -1.6      0.7    0      0  0 0 0 0 0 0 0 0 C 3 0 -1 0 0 0 0 0 0 [C]
32                         4      C      10      0      0      1.3   -1.1        0    0      0                    0000000C40-1000000[C]
33                         5      C      10      0      0      1.2   0.48        0    0      0  0 0 0 0 0 0 0 0 C 5 0 -1 0 0 0 0 0 0 [C]
34                         6      C      10      0      0        0   1.01       -1    0      0  0 0 0 0 0 0 0 0 C 6 0 -1 0 0 0 0 0 0 [C]
35                         7      O      45      0      0        0   2.42       -1    0      0  0 0 0 0 0 0 0 0 O 7 0 -1 0 0 0 0 0 0 [O]
36                         8      H       8      0      0      0.6   2.72       -1    0      0  0 0 0 0 0 0 0 0 H 7 0 -1 0 0 0 0 0 0 [H]
37                         9      H       1      0      0      2.1   0.86       -1    0      0  0 0 0 0 0 0 0 0 H 8 0 -1 0 0 0 0 0 0 [H]
38                        10      H       1      0      0      1.4   0.86      0.8    0      0  0 0 0 0 0 0 0 0 H 9 0 -1 0 0 0 0 0 0 [H]
39                        11      H       1      0      0      1.1   -1.4       -1    0      0    0 0 0 0 0 0 0 0 H 10 0 -1 0 0 00 00[H]
40                        12      H       1      0      0      2.2   -1.4      0.2    0      0    0 0 0 0 0 0 0 0 H 11 0 -1 0 0 0000 [H]
41                        13      H       1      0      0        0   0.72       -2    0      0    0 0 0 0 0 0 0 0 H 12 0 -1 0 0000 0 [H]
42                        14      H       1      0      0      0.1   -2.7      0.7    0      0    0 0 0 0 0 0 0 0 H 13 0 -1 0 0 0000 [H]
```

```
43                          15      H       1     0     0      0.3   -1.3     1.7   0     0    0 0 0 0 0 0 0 H 14 0 -1 0 0 00 [H]
44                          16      H       1     0     0       -1   -1.5      -1   0     0    0 0 0 0 0 0 0 H 15 0 -1 0 0 0000 [H]
45                          17      H       1     0     0       -2   -1.5     0.9   0     0    0 0 0 0 0 0 0 H 16 0 -1 0 0 0000 [H]
46                          18      H       1     0     0       -1   0.85     1.2   0     0    0 0 0 0 0 0 0 H 17 0 -1 0 0 0000 [H]
47                          19      H       1     0     0       -2   0.83       0   0     0    0 0 0 0 0 0 0 H 18 0 -1 0 0 0000 [H]
48                                * Bond List
49                                      * Bond# bond_type atom1 atom2 cis/trans length locked ring Sh_type Sh_nr Qorder Qtopol Qs
50                          1 1 1 2 0                                0.000 0 0 0 0 [S] 0 0
51                          2 1 1 6 0                    0.000 0 0 0 0 [S] 0 0
52                                 3 1 1 18 0                    0.000 0 0 0 0 [S] 0 0
53                                 4 1 1 19 0                    0.000 0 0 0 0 [S] 0 0
54                          5 1 2 3 0                    0.000 0 0 0 0 [S] 0 0
55                                 6 1 2 16 0                    0.000 0 0 0 0 [S] 0 0
56                                 7 1 2 17 0                    0.000 0 0 0 0 [S] 0 0
57                          8 1 3 4 0                    0.000 0 0 0 0 [S] 0 0
58                                 9 1 3 14 0                    0.000 0 0 0 0 [S] 0 0
59                                10 1 3 15 0                    0.000 0 0 0 0 [S] 0 0
60                                 11 1 4 5 0                    0.000 0 0 0 0 [S] 0 0
61                                12 1 4 11 0                    0.000 0 0 0 0 [S] 0 0
62                                13 1 4 12 0                    0.000 0 0 0 0 [S] 0 0
63                                 14 1 5 6 0                    0.000 0 0 0 0 [S] 0 0
64                                       15 1 5 9 0                    0.000 0 0 0 0 [S] 0 0
65                                16 1 5 10 0                    0.000 0 0 0 0 [S] 0 0
66                                 17 1 6 7 0                    0.000 0 0 0 0 [S] 0 0
67                                18 1 6 13 0                    0.000 0 0 0 0 [S] 0 0
68                                 19 1 7 8 0                    0.000 0 0 0 0 [S] 0 0
69                               * Bond Angles
70                                           * bond1 bond2 angle locked
71                                 * Dihedral Angles
```

```
72                              * at1-cons at1 at2 at2-cons angle locked
73                                 * Planarity data
74                                 * User data area
75                              * End of File
```

The MSI MolFile[1] format is broken up into several sections. Section headers are preceded by a "*". Blank lines also contain a "*". Each line is either a blank line, a header line or a data record containing one or more fields of information about the structure. Individual fields are delimited by space(s) or a tab. The fields in the MSI MolFile format file used by Chem3D Proare discussed below.
The field value for Carbon 6 from the example file is included in parentheses for reference:

1. Line 1 is a standard header line for MSI MolFile format files.
2. Line 2 normally indicates the application which created the file.
3. Line 3 is the header for the File format version number section.
4. Line 4 indicates the file format version number. The format for this field is YY.MMDD.
5. Line 5 is the header for the File update version number section.
6. Line 6 indicates the file update version number. The format for this field is YY.MMDD.
7. Line 7 is the header for the molecule name section.
8. Line 8 contains the field molecule name. This field contains either the file name, or "Undefined Name".
9. Line 9 is the header for the empirical formula.
10. Line 10 contains the empirical formula field. This field contains either the empirical formula or "Undefined Empirical Formula".
11. Lines 11–24 each contains information concerning conversions from 3D to 2D.
12. Line 25 is the header for the Global display attributes section.
13. Line 26 contains 5 fields describing the global display attributes: Line thickness (1), font style (0), type face (1), type size (12), font (256). These values are specific to the platform that is generating the file.
14. .Line 27 contains the header for the Atom Lists section.
15. Line 28 contains a listing of all the possible fields for the atom list section. When the file is created using Chem3D Pro the following fields are used: Atom#,Lbl, Type, and x,y,z.
16. Lines 29–47 each contains 28 fields describing information about each of the atoms in the structure: the first field is the atom number (6), the second field is the atom label (C), the third field is the atom type (10), the fourth field and fifth fields contain 2D coordinates, and contain zeros when the file is created using Chem3D Pro, the sixth field is the X coordinate (-0.113) and the fifth field is the Y coordinate (1.005), the sixth field is the Z coordinate (-0.675), the seventh through fifteenth fields are ignored and contain zeros when the file is created by Chem3D Pro, the

[1]Molecular Simulations MOLFILE (ChemNote) is a product of Molecular Simulations, Inc.

sixteenth field is, again, the atom label (C), the eighteenth field is, again, the atom number (6), the nineteenth field is the segment field, the twentieth field is the coordination field, the twenty first field is ignored, the twenty-second field is called the saturation field: if the atom is attached to any single, double or delocalized bonds this field is 1 (not saturated) otherwise this field is 0. The twenty-third through the twenty-sixth fields are ignored and contain zeros when the file is created using Chem3D Pro, the twenty-seventh field is, again, the atom label (C).

Note: *Atom types in the Molecular Simulations MolFile format are user-definable. For more information, see* *"Editing file format atom types" on page 250.*

17. Line 48 contains the header for the Bond List section.
18. Line 49 contains a listing of all the possible fields for the bond list section. When the file is created by Chem3D Prothe following fields are used: Bond#, Bond_type, atom 1, atom 2 and cis/trans and Qorder.
19. Lines 50–68 each contain 4 fields describing information about each of the bonds in the structure: the first field is the internal bond number (6), the second field is the bond type (1), the third and fourth fields are the atom serial numbers for the atoms involved in the bond [atom 1 (2), atom 2 (16)], the fifth field is the cis/trans designator (this is 0 if it does not apply), the sixth through tenth fields are ignored, and contain zeros if the file is created using Chem3D Pro, the eleventh field contains the bond order ([S] meaning single), the twelfth and thirteenth fields are ignored and contain zeros if the file is created using Chem3D Pro.
20. Lines 69–73 are each a section header for 3D conversion use. This section only contains the header name only (as shown) when the file is created using Chem3D Pro.
21. Line 74 is a header for the section User data area. This section contains the header name only (as shown) when the file is created using Chem3D Pro.
22. Line 75 is a header that indicates the End of File.

FORTRAN formats. The FORTRAN format for each record of the Molecular Simulations MolFile format is as follows:

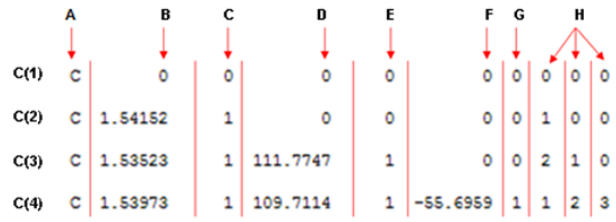
Line Number	Description	FORTRAN Format
29-47	atom list, field value	I,1X,A,3(1X,I),3F9.3,1X,I,F4.1,7(1X,I),1X,A,I,8(1X,I), "[",A, "] "
50-68	bond list, field values	I,4(1X,I),F9.3,4(2X,I),1X, "[",A1, "] ",2(1X,I)

MOPAC

ChemBio3D uses the MOPAC Data-File format. This format is described on pages 1-5 through 1-7 in the "Description of MOPAC" section and page 3-5 in the "Geometry Specification" section in the MOPAC Manual (fifth edition). For further details about the MOPAC Data-File format, please refer to the above publication.
The table below is a sample MOPAC output file from ChemBio3D for cyclohexanol:

```
 Line 1:

 Line 2:          MyCyclohexanolModel.mop

 Line 3:

Line 4a:     C       0     0        0     0        0 0 0 0 0

Line 4b:     C 1.54152     1        0     0        0 0 1 0 0

Line 4c:     C 1.53523     1 111.7747     1        0 0 2 1 0

Line 4d:     C 1.53973     1 109.7114     1 -55.6959 1 1 2 3

Line 4e:     C 1.53597     1 111.7012     1  55.3112 1 4 1 2

Line 4f:     C 1.53424     1 110.7535     1 57.03175 1 3 2 1

Line 4g:     O 1.40196     1 107.6989     1 -172.662 1 1 2 3

Line 4h:     H 1.11739     1 107.8685     1 62.06751 1 1 2 3

Line 4I:     H 1.11633     1 110.0751     1  -177.17 1 2 1 4

Line 4j:     H 1.11566     1 109.4526     1 65.43868 1 2 1 4

Line 4k:     H 1.11665     1 109.9597     1 178.6209 1 3 2 1

Line 4l:     H  1.1161     1 109.5453     1 -63.9507 1 3 2 1

Line 4m:     H 1.11542     1 109.4316     1 -66.0209 1 4 1 2

Line 4n:     H 1.11499     1  110.549     1 176.0838 1 4 1 2

Line 4o:     H 1.11671     1   109.93     1 -178.296 1 5 4 1

Line 4p:     H 1.11615     1 109.4596     1 64.43501 1 5 4 1

Line 4q:     H 1.11664     1 110.0104     1 -178.325 1 6 3 2

Line 4r:     H 1.11604     1 109.6082     1 64.09581 1 6 3 2

Line 4s:     H 0.94199     1  106.898     1 -173.033 1 7 1 2
```

The following illustrates the components of the MOPAC Output File from ChemBio3D for C(1) Through C(4) of Cyclohexanol



The internal coordinates section of the MOPAC Data-File format contains one line of text for each atom in the model. Each line contains bond lengths, bond angles, dihedral angles, action integers, and connectivity atoms.

As shown in the illustration above, C(1) is the origin atom. C(2) is connected to C(1) with a bond of length 1.54152 Å. C(3) is connected to C(2) with a bond of length 1.53523 Å, and is at a bond angle of 111.7747 degrees from C(1). C(4) is connected to C(1) with a bond of length 1.539734 Å, and is at a bond angle of 109.711411 degrees from C(2). C(4) also forms a dihedral angle of
-55.6959 degrees with C(3).
The action integers listed next to each measurement are instructions to MOPAC:

`1` Optimize this internal coordinate
`0` Do not optimize this internal coordinate
`-1` Reaction coordinate or grid index

When you create a MOPAC file in ChemBio3D, an action integer of 1 is assigned to each non-zero bond length, bond angle, and dihedral angle for each atom record in the file.
FORTRAN Formats. The description of the MOPAC Data-File format for each line is:

Line Number	Description	Read by Chem-Bio3D	Written by Chem-Bio3D
1	Keywords for Calculation Instructions	No	No
2	Molecule Title	No	Yes
3	Comment	No	No
4a-s	Internal coordinates for molecule	Yes	Yes
5	Blank line, terminates geometry definition	Yes	Yes
The FORTRAN format for each line containing internal coordinate data in the MOPAC Data-File is FORMAT(1X, 2A, 3(F12.6, I3), 1X, 3I4).			

Protein Data Bank files

The Protein Data Bank file format (Protein DB) is taken from pages 3, 14–15, and 17–18 of the Protein Data Bank Atomic coordinate and Bibliographic Entry Format Description dated January, 1985.
A Protein Data Bank file can contain as many as 32 different record types. Only the COMPND, ATOM, HETATM, and CONECT records are used by ChemBio3D; all other records in a Protein Data Bank file are ignored. The COMPND record contains the name of the molecule and identifying information.
The ATOM record contains atomic coordinate records for “standard” groups, and the HETATM record contains atomic coordinate records for “non-standard” groups. The CONECT record contains the atomic connectivity records.

Note: *The COMPND record is created by ChemBio3D to include the title of a ChemBio3D model only when you are saving a file using the Protein Data Bank file format. This record is not used when opening a file.*

The following is an example of a Protein Data Bank Output File from ChemBio3D for L-Alanine.

COMPND			**Alanine.pdb**		
HETATM	1	N	0	-0.962	1
HETATM	2	C	0	-0.049	0
HETATM	3	C	0.6	0.834	-1
HETATM	4	C	-2	0.834	1
HETATM	5	O	0.3	1.737	-1
HETATM	6	O	1.8	0.459	0
HETATM	7	H	0.9	-1.398	1
HETATM	13	H	-1	-1.737	1
HETATM	8	H	-1	-0.642	-1
HETATM	9	H	-2	1.564	0
HETATM	10	H	-1	1.41	1
HETATM	11	H	-2	0.211	1
HETATM	12	H	2.4	1.06	-1
CONECT	1	2	7	13	
CONECT	2	1	3	4	8
CONECT	3	2	5	6	
CONECT	4	2	9	10	11
CONECT	5	3			
CONECT	6	3	12		
CONECT	7	1			
CONECT	13	1			
CONECT	8	2			
CONECT	9	4			
CONECT	10	4			
CONECT	11	4			
CONECT	12	6			
END					

The ATOM or HETATM record contains the record name, followed by the serial number of the atom being described, the element symbol for that atom, then the X, Y, and Z Cartesian coordinates for that atom.
A CONECT record is used to describe the atomic connectivity. The CONECT records contain the record name, followed by the serial number of the atom whose connectivity is being described, then the serial numbers of the first atom, second atom, third atom and fourth atom to which the described atom is connected.

FORTRAN formats. The full description of the COMPND record format in Protein Data Bank files is as follows:

Column Number	Column Description	Used by ChemBio3D?
1-6	Record Name (COMPND)	Yes
7-10	UNUSED	No
11-70	Name of Molecule	Yes

The description of the ATOM and HETATM record formats in Protein Data Bank files is:

Column Number	Column Description	Used by ChemBio3D?
1-6	Record Name (HETATM or ATOM)	Yes
7-11	Atom Serial Number	Yes
12	UNUSED	No
13–16	Atom Name (Element Symbol)	Yes
17	Alternate Location Indicator	No
18–20	Residue Name	Optional
21	UNUSED	No
22	Chain Identifier	No
23–26	Residue Sequence Number	No
27	Code for insertions of residues	No
28–30	UNUSED	No
31–38	X Orthogonal Å coordinates	Yes

39–46	Y Orthogonal Å coordinates	Yes
47–54	Z Orthogonal Å coordinates	Yes
55–60	Occupancy	No
61–66	Temperature Factor	No
67	UNUSED	No
68–70	Footnote Number	No

The full description of the CONECT record format in Protein Data Bank files is as follows:

Column Number	Column Description	Used by ChemBio3D?
1–6	Record Name (CONECT)	Yes
7–11	Atom Serial Number	Yes
12–16	Serial Number of First Bonded Atom	Yes
17–21	Serial Number of Second Bonded Atom	Yes
22–26	Serial Number of Third Bonded Atom	Yes
27–31	Serial Number of Fourth Bonded Atom	Yes
32–36	Hydrogen Bonds, Atoms in cols. 7–11 are Donors	No
37–41	Hydrogen Bonds	No
42–46	Salt Bridge, Atoms in cols. 7–11 have Negative Charge	No
47–51	Hydrogen Bonds, Atoms in cols 7–11 are Acceptors	No
52–56	Hydrogen Bonds	No
57–61	Salt Bridge, Atoms in cols. 7–11 have Positive Charge	No

The FORTRAN formats for the records used in the Protein Data Bank file format are as follows:

Line Description	FORTRAN Format
COMPND	'COMPND', 4X, 60A1
ATOM	'ATOM', 2X, I5,1X,A4, 1X, A3,10X, 3F8.3,16X
HETATM	'HETATM', I5,1X,A4,14X,3F8.3,16X
CONECT	'CONECT', 5I5, 30X

ROSDAL

The ROSDAL (Representation of Organic Structures Description Arranged Linearly) Structure Language[1] file format is defined in Appendix C: Rosdal Syntax, pages
91–108, of the MOLKICK User's Manual. The Rosdal format is primarily used for query searching in the Beilstein Online Database. Rosdal format files are for export only. The following is a sample Rosdal format file created using Chem3D Pro for cyclohexanol:
1-2-3-4-5-6,1-6,2-7H,3-8H,4-9H,5-10H,6-11H,1-12O-13H,1-14H,2-15H, 3-16H,4-17H,5-18H,6-19H.@

SMD

The Standard Molecular Data [2]SMD file) file format is defined in the SMD File Format version 4.3 documentation, dated 04-Feb-1987. The following is a sample SMD file produced using Chem3D Pro for cyclohexanol (the line numbers are added for purposes of discussion only).

```
Line 1 >STRT Cyclohexane
Line 2 DTCR Chem3D 00000 05-MAY-92 12:32:26
Line 3      >CT Cyclohexan 00039
 Line 4       19 19 (A2,5I2) (6I3)
 Line 5       C          0        0        0
 Line 6        C         0        0        0
```

[1]Rosdal is a product of Softron, Inc.
[2]SMD format - H. Bebak AV-IM-AM Bayer AG.

Line 7	C	0	0	0
Line 8	C	0	0	0
Line 9	C	0	0	0
Line 10	C	0	0	0
Line 11	H	0	0	0
Line 12	H	0	0	0
Line 13	H	0	0	0
Line 14	H	0	0	0
Line 15	H	0	0	0
Line 16	O	0	0	0
Line 17	H	0	0	0
Line 18	H	0	0	0
Line 19	H	0	0	0
Line 20	H	0	0	0
Line 21	H	0	0	0
Line 22	H	0	0	0
Line 23	H	0	0	0
Line 24	1	2	1	
Line 25	1	6	1	
Line 26	1	12	1	
Line 27	1	14	1	
Line 28	2	3	1	
Line 29	2	7	1	
Line 30	2	15	1	
Line 31	3	4	1	
Line 32	3	8	1	
Line 33	3	16	1	
Line 34	4	5	1	
Line 35	4	9	1	
Line 36	4	17	1	
Line 37	5	6	1	
Line 38	5	10	1	

```
Line 39         5        18         1
Line 40         6        11         1
Line 41         6        19         1
Line 42        12        13         1
Line 43                   >CO ANGSTROEM 0020
Line 44         4    (3I10)
Line 45     -6903     13566     -4583
Line 46    -14061       808       125
Line 47     -4424     -8880      7132
Line 48      7577    -12182     -1855
Line 49     14874       594     -6240
Line 50      5270     10234    -13349
Line 51    -18551     -4300     -8725
Line 52     -9815    -18274      9852
Line 53      4047    -17718    -10879
Line 54     19321      5600      2685
Line 55     10636     19608    -16168
Line 56     -2794     21139      6600
Line 57      2876     15736     11820
Line 58    -14029     20018    -10310
Line 59    -22477      3450      6965
Line 60      -806     -4365     16672
Line 61     14642    -18918      3566
Line 62     23341     -2014    -13035
Line 63      1740      5536    -22837
```

Each line is either a blank line, a block header line or a data record containing multiple fields of information about the structure. The SMD file is broken down into several blocks of information. The header for each block starts with a > sign. Individual fields are delimited by space(s) or a tab.

The fields in the SMD format file used by Chem3D Pro are discussed below:

1. Line 1 starts the block named STRT. This block contains the molecule name. The molecule name is the file name when the file was created using Chem3D Pro.
2. Line 2 starts the block named DTCR. The information in this line includes the name of the application that created the file and the date and time when the file was generated.

3. Line 3 starts the block named CT which contains the connection table of the compound(s). Also on this line is a 10 character description of the connection table. This will be the same as the file name when the file is generated using Chem3D Pro. Finally, the number of records contained within the CT block is indicated, 39 in the above example.
4. Line 4 of the CT Block contains four fields. The first field is the number of atoms, the second field is the number of bonds, the third field is the FORTRAN format for the number of atoms, and the fourth field is the FORTRAN format for the number of bonds.
5. Lines 5–23 of the CT Block each contain 4 fields describing an atom. The first field is the element symbol (first letter uppercase, second lowercase). The second field is the total number of hydrogens attached to the atom, the third field is the stereo information about the atom and the fourth field is the formal charge of the atom.

Note: *If the file is created using Chem3D Pro, the number of hydrogens, the stereo information and the formal charge fields are not used, and will always contain zeros.*

6. Lines 24–42 of the CT Block each contains 3 fields describing a bond between the two atoms. The first field is the serial number of the atom from which the bond starts, the second field is the serial number of atom where the bond ends, and the third field is the bond order.
7. Line 43 starts the block named CO, The information in this block includes the Cartesian coordinates of all the atoms from the CT block and indicates the type of coordinates used, Angstroms in this example. Also in this line is the number of lines in the block, 20 in this example.
8. Line 44 contains two fields. The first field contains the exponent used to convert the coordinates in the lines following to the coordinate type specified in line 43. The second field is the FORTRAN format of the atom coordinates.
9. Lines 45–65 each contains three fields describing the Cartesian coordinates of an atom indicated in the CT block. The first field is the X coordinate, the second field is the Y coordinate and the third field is the Z coordinate.

SYBYL MOL file

The SYBYL MOL File format (SYBYL) is defined in Chapter 9, “SYBYL File Formats”, pages 9–1 through 9–5, of the *1989 SYBYL Programming Manual*.

The table below is an example of a file in SYBYL format produced in ChemBio3D. This file describes a model of cyclohexanol.

```
19 MOL  Cyclohexanol0
  1   1   1.068  0.3581 -0.7007C
  2   1 -0.207  1.2238 -0.7007C
  3   1 -1.473  0.3737 -0.5185C
  4   1 1.1286  -0.477   0.5913C
  5   1 -0.139  -1.324   0.7800C
```

```
  6   1 -1.396 -0.445  0.7768C
  7   8 2.1708 1.2238 -0.7007O
  8  13 1.0068 -0.343 -1.5689H
  9  13 -0.284 1.7936 -1.6577H
 10  13 -0.147 1.9741  0.1228H
 11  13 -2.375  1.032 -0.4983H
 12  13 -1.589 -0.314 -1.3895H
 13  13 1.2546  0.202  1.4669H
 14  13 2.0091 -1.161  0.5742H
 15  13 -0.077 -1.893  1.7389H
 16  13  -0.21 -2.076 -0.0419H
 17  13 -2.308 -1.081  0.8816H
 18  13 -1.372 0.2442  1.6545H
 19  13 2.9386 0.6891 -0.8100H
 19 MOL
  1   1      2       1
  2   1      4       1
  3   1      7       1
  4   1      8       1
  5   2      3       1
  6   2      9       1
  7   2     10       1
  8   3      6       1
  9   3     11       1
 10   3     12       1
 11   4      5       1
 12   4     13       1
 13   4     14       1
 14   5      6       1
 15   5     15       1
 16   5     16       1
 17   6     17       1
```

```
18   6     18       1

19   7     19       1

 0 MOL
```

The following illustration shows the components of the SYBYL Output File from ChemBio3D for C(6) and Bond 3 of Cyclohexanol.

The format for SYBYL MOL files is as follows:

1. The first record in the SYBYL MOL File contains the number of atoms in the model, the word “MOL”, the name of the molecule, and the center of the molecule.
2. The atom records (lines 2–20 in the cyclohexanol example) contain the Atom ID in column 1, followed by the Atom Type in column 2, and the X, Y and Z Cartesian coordinates of that atom in columns 3–5.
3. The first record after the last atom records contains the number of bonds in the molecule, followed by the word “MOL”.
4. The bond records (lines 22–40 in the cyclohexanol example) contain the Bond Number in column 1, followed by the Atom ID of the atom where the bond starts (the “From-Atom”) in column 2 and the Atom ID of the atom where the bond stops (the “To-Atom”) in column 3. The last column in the bond records is the bond type. Finally the last line in the file is the Number of Features record, which contains the number of feature records in the molecule. Chem-Bio3D does not use this information.

FORTRAN formats. The FORTRAN format for each record of the SYBYL MOL File format is as follows:

Line Description	FORTRAN Format
Number of Atoms/File Name	I4,1X,'MOL',20A2,11X,I4
Atom records	2I4,3F9.4,2A2
Number of Bonds record	I4,1X,'MOL'
Bond records	3I4,9X,I4
Number of Features record	I4,1X,'MOL'

SYBYL MOL2 file

The SYBYL MOL2[1] file format (SYBYL2) is a portable representation of a SYBYL molecule. The file, which is in ASCII format, contains all the information necesary to construct the molecule. The sample file shown below of cyclo-hexanol was created using ChemBio3D Ultra:

```
                ****
   19     19        1        0        0
 SMALL
 USER_CHARGES


@<TRIPOS>ATOM


     1       C  00.8340  -0.2126  0.9718     C.3   1  **** 0.0000
     2       C   0.5916  -1.3023  -0.0691    C.3   1  **** 0.0000
     3       C  -0.8165  -1.2202  -0.6525    C.3   1  **** 0.0000
     4       C  -1.1138   0.1685  -1.2118    C.3   1  **** 0.0000
     5       C  -0.8714   1.2582  -0.1708    C.3   1  **** 0.0000
     6       C   0.5366   1.1760   0.4125    C.3   1  **** 0.0000
     7       O   2.1753  -0.2616   1.3768    O.3   1  **** 0.0000
     8       H   0.1512  -0.3949   1.8316      H   1  **** 0.0000
     9       H   1.3306  -1.1849  -0.8930      H   1  **** 0.0000
    10       H   0.7044  -2.2910   0.4295      H   1  **** 0.0000
    11       H  -0.9114  -1.9670  -1.4722      H   1  **** 0.0000
    12       H  -1.5439  -1.4296   0.1636      H   1  **** 0.0000
    13       H  -0.4530   0.3535  -2.0880      H   1  **** 0.0000
    14       H  -2.1863   0.2022  -1.5074      H   1  **** 0.0000
    15       H  -1.0049   2.2529  -0.6521      H   1  **** 0.0000
    16       H  -1.6002   1.1157   0.6583      H   1  **** 0.0000
    17       H   1.2732   1.4072  -0.3894      H   1  **** 0.0000
    18       H   0.6114   1.9100   1.2458      H   1  **** 0.0000
```

[1]SYBYL is a product of TRIPOS.

```
     19      H   2.2933   0.4198   2.0164      H   1  **** 0.0000

        @<TRIPOS>BOND

      1      1        2        1

      2      1        6        1

      3      1        7        1

      4      1        8        1

      5      2        3        1

      6      2        9        1

      7      2       10        1

      8      3        4        1

      9      3       11        1

     10      3       12        1

     11      4        5        1

     12      4       13        1

     13      4       14        1

     14      5        6        1

     15      5       15        1

     16      5       16        1

     17      6       17        1

     18      6       18        1

     19      7       19        1
```

Each line is either a blank line, a section header or a data record containing multiple fields of information about the compound. The SYBYL MOL2 file is broken down into several sections of information. Record type indicators (RTI) break the information about the molecule into sections. RTI's are always preceded by an "@" sign. Individual fields are delimited by space(s) or a tab.

The fields in the SYBYL MOL2 format file used by Chem3D Proare as follows:

1. Line 1 is a comment field. The pound sign preceding the text indicates a comment line. Name: is a field designating the name of molecule. The molecule name is the file name when the file is created using Chem3D Pro.
2. Line 2 is a blank line.
3. Line 3, "@<TRIPOS>MOLECULE", is a Record Type Indicator (RTI) which begins a section containing information about the molecule(s) contained in the file.

Note: *There are many additional RTIs in the SYBYL MOL2 format. Chem3D Pro uses only @<TRIPOS>MOLECULE, @<TRIPOS>ATOM and @<TRIPOS>BOND.*

4. Line 4 contains the name of the molecule. The name on line 4 is the same as the name on line 1.

5. Line 5 contains 5 fields describing information about the molecule: The first field is the number of atoms, the second field is the number of bonds, the third field is the number of substructures, the fourth field is the number of features and the fifth field is the number of sets.

📝 ***Note:*** *Chem3D Pro ignores the following fields: number of substructures, number of features and number of sets. These fields will contain zeros if the file was created using Chem3D Pro.*

6. Line 6 describes the molecule type. This field contains SMALL if the file is created using Chem3D Pro.
7. Line 7 describes the charge type associated with the molecule. This field contains NO_CHARGES if the file is created using Chem3D Pro.
8. Line 8, blank in the above example, might contain internal SYBYL status bits associated with the molecule.
9. Line 9, blank in the above example, might contain comments associated with the molecule.

📝 ***Note:*** *Four asterisks appear in line 8 when there are no status bits associated with the molecule but there is a comment in Line 9.*

10. Line 10, "@<TRIPOS>ATOM", is a Record Type Indicator (RTI) which begins a section containing information about each of the atoms associated with the molecule.
11. Lines 11–29 each contain 6 fields describing information about an atom: the first field is the atom id, the second field is the atom name, the third field is the X coordinate, the fourth field is the Y coordinate, the fifth field is the Z coordinate and the sixth field is the atom type.

📝 ***Note:*** *Atom types are user-definable See "Editing file format atom types" on page 250 for instructions on modifying or creating an atom type.*

12. Line 30, "@<TRIPOS>BOND", is a Record Type Indicator (RTI) which begins a section containing information about the bonds associated with the molecule.
13. ..Lines 31–49 each contain 4 fields describing information about a bond: the first field is the bond id, the second field is the from-atom id, the third field is the to-atom id, and the fourth field is the bond type.

FORTRAN formats. The FORTRAN format for each record of the SYBYL MOL2 File format is as follows:

Line Number	Description	FORTRAN Format
1	Molecule name (file name)	"# ",5X, "Name: ",1X,A
5	Number of atoms/number of bonds	4(1X,I2)
11–29	Atom type, name, coordinates and id	I4,6X,A2,3X,3F9.3,2X,A5
31–49	Bond id, from-atom, to-atom, bond type	3I4,3X,A2

Export file formats

The following table shows all of the chemistry file formats that ChemBio3D 13.0 supports.

File Format	Name	Extension
Alchemy	Alchemy	.alc; .mol
Cartesian Coordinate	Cart Coords 1	.cc1
	Cart Coords 2	.cc2
CCDB	Cambridge Crystallographic Database	.ccd
Chem3D		.c3xml; .c3d
Chem3D template		.c3t
ChemDraw	ChemDraw	.cdx; .cdxml
Connection Table	Conn Table	.ct; .con
CS GAMESS Input	CS GAMESS Input	.inp
Gaussian Checkpoint		.fchk; .fch
Gaussian Cube		.cub
Gaussian Input	Gaussian Input	.gjc; .gjf
Internal Coordinates	Int Coords	.int
MacroModel	MacroModel	.mcm; .dat; .out
Maestro	Maestro	*.mae
Molecular Design Limited MolFile	MDL MolFile	.mol
MSI ChemNote	MSI ChemNote	.msm
MOPAC input file	MOPAC	.mop; .dat; .mpc; 2mt

File Format	Name	Extension
MOPAC graph file		.gpt
Protein Data Bank	Protein DB	.pdb; .ent
ROSDAL	Rosdal	.rdl
Standard Molecular Data	SMD File	.smd
SYBYL MOL	SYBYL	.sml
SYBYL MOL2	SYBYL2	.sm2; .ml2

To save a model with a different format, name or location:

1. Go to **File**>**Save As**. The Save File dialog box appears.
2. Specify the name of the file, the folder, and where you want to save the file.
3. Select the file format in which you want to save the model.
4. Click **Save**.

When you save a file in another file format, only information relevant to the file format is saved. For example, you will lose dot surfaces, color, and atom labels when saving a file as an MDL MolFile.

Publishing formats

The file formats described in this section are available for importing and exporting models as pictures. The pictures can then be used in desktop publishing and word processing software.

Image format features

- Transparent OLE copy/paste
- Save bitmap images up to 1200 DPI.
- JPEG Quality (compression) can be adjusted from 0 to 100%.
- Movies can be saved in animated GIF, multi-page TIFF, or AVI formats.

The defaults are set in the new **Pictures** tab of the Preferences dialog box.
The Save As dialog box now displays the available options, to make it easier to override defaults when you save.

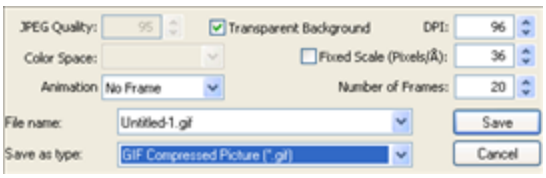


Figure 14.4: Save as GIF dialog box.

Graphic file formatting uses CxImage©, an open source toolset under the zlib license.[1]

WMF and EMF. ChemBio3D supports the Windows Metafile and Enhanced Metafile file formats. These are the only graphic formats (as opposed to chemistry modeling formats) that can be used for import. They may also be used for export, EMF by using the **Save As...** File menu command or the clipboard, and WMF by using the clipboard (only). See "Copying as a static image" on page 29 for more information. EMF files are exported with transparent backgrounds, when this is supported by the operating system (Windows 2000 and Windows XP). The WMF and EMF file formats are supported by applications such as Microsoft Word for Windows.

Note: *ChemBio3D 13.0 does not embed structural information in models exported as EMF files. If you have EMF files produced with previous versions, you can still open them in ChemBio3D 13.0 and work with the structure. However, EMF files saved from Chem3D 8.0 contain graphic information only and cannot be opened in ChemBio3D 13.0.*

BMP. The Bitmap file format saves the bitmapped representation of a ChemBio3D picture. The Bitmap file format enables you to transfer ChemBio3D pictures to other applications, such as Microsoft Word for Windows, that support bitmaps.

EPS. The PostScript file format saves models as encapsulated postscript file (EPS). EPS files are ASCII text files containing the scalable PostScript representation of a ChemBio3D picture. You can open EPS files using other applications such as PageMaker. You can transfer EPS files among platforms, including Macintosh, Windows, and UNIX.

TIF. The Tagged Image File Format (TIFF) contains binary data describing a bitmap image of the model. TIFF is a high resolution format commonly used for saving graphics for cross-platform importing into desktop publishing applications. TIFF images can be saved using a variety of resolution, color, and compression options. As TIFF images can get large, choosing appropriate options is important.

When you save a file as TIF, an option button appears in the Save As dialog box.

To specify the save options:

1. Click **Options**.

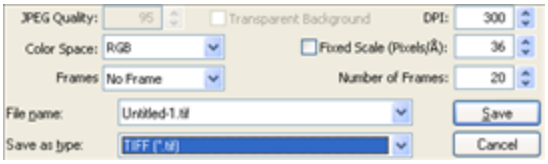


Figure 14.5: The TIFF Options dialog box.

2. Choose a resolution. The size of the file increases as the square of the resolution.
3. Choose a color option.

[1] CxImage: Copyright © 2001 - 2004, David Pizzolato

If you want to …	Then choose …
force objects to black and white.	**Monochrome.**
store colors using computer monitor style of color encoding.	**RGB Indexed.**
use printing press style of color encoding.	**CMYK Contiguous.** Stores colors non-sequentially. For example: CMYKCMYK. The PackBits compression type provides no compression for this type of file.

Note: *If objects in your document are black and white they are saved as black and white regardless of which Color options you set. If you import drawings from other applications and want them to print Black and White you must set the Color option to Monochrome.*

4. Choose a compression option:

PackBits.. reduce file size by encoding repeating bytes of information as output. For example, for a line of color information such as: CCCCCMMMMMYYYYYKKKKK, the compression yields a smaller file by representing the information as C5M5Y5K5.

CCITT Group 3 or CCITT Group 4.. fax transmissions of images

GIF, PNG and JPG. Use the Graphics Interchange Format (GIF), Portable Network Graphics (PNG) file format, or the JPEG format to publish a ChemBio3D model on the world wide web. Each of these formats uses a compression algorithm to reduce the size of the file. Applications that can import GIF, PNG, and JPG files include Netscape Communicator and Microsoft Internet Explorer.

The model window background color is used as the transparent color in the GIF format graphic.

Note: *The size of the image in ChemBio3D when you save the file will be the same in your Web page. If you turn on the "Fit Model to Window" building preference, you can resize the window in ChemBio3D to resize the model then save.*

3DM. The QuickDraw 3D MetaFile (3DM) file format contains 3-dimensional object data describing the model. You can import 3DM files into many 3D modeling applications. You can transfer 3DM files between Macintosh and Windows platforms.

AVI. Use this file format to save a movie you have created for the active model. You can import the resulting movie file into any application that supports the AVI file format.

Export formats

The following file formats are used to export models to chemistry modeling application other than ChemBio3D 13.0. Most of the formats also support import.

Alchemy
Use the ALC file format to interface with TRIPOS© applications such as Alchemy©. This is supported only for input.

Cartesian Coordinates
Use Cartesian Coordinates 1 (.CC1) or 2 (.CC2) to import or export the X, Y, and Z Cartesian coordinates for your model.
When you save a file as Cartesian Coordinates, an option button appears in the Save As dialog box.
To specify the save options:

1. Click **Save As**.
2. Select Cartesian Coordinate format (.cc1 or .cc2) in the Save As dialog box.
3. Select from these options:

By Serial Number. Contain a connection table for each atom with serial numbers.
By Position. Contain a connection table for each atom that describes adjacent atoms by their positions in the file.
Missing. Not contain a connection table
Include Serial Numbers. Contain serial numbers.
Include Atom Type Text Numbers. Contain atom type numbers.
Save All Frames. Contain internal coordinates for each view of the model.

Connection Table
ChemBio3D uses the atom symbols and bond orders of connection table files to guess the atom symbols and bond orders of the atom types. There are two connection table file formats, CT and CON. The CON format is supported only for import.
When you save a file as a Connection Table, an Options button appears in the Save As dialog box.
To specify the save options:

1. Click **Save As**.
2. Select the Conn Table format in the Save As dialog box.
3. Select from these options:

1 Blank Line. add a blank line to the top of the file.
2 Blank Lines. add two blank lines to the top of the file.
3 Blank Lines. add three blank lines to the top of the file.

Gaussian Input
Use the Gaussian Input (GJC, GJF) file format to interface with models submitted for Gaussian calculations. Either file format may be used to import a model. Only the Molecule Specification section of the input file is saved. For atoms not otherwise specified in ChemBio3D, the charge by default is written as 0, and the spin multiplicity is written as 1. You can edit Gaussian Input files using a text editor with the addition of keywords and changing optimization flags for running the file using the Run Gaussian Input file within ChemBio3D, or using Gaussian directly.

Gaussian Checkpoint

A Gaussian Checkpoint file (FCHK; FCH) stores the results of Gaussian Calculations. It contains the final geometry, electronic structure (including energy levels) and other properties of the molecule. Checkpoint files are supported for import only.

ChemBio3D displays atomic orbitals and energy levels stored in Checkpoint files. If Cubegen is installed, molecular surfaces are calculated from the Checkpoint file.

Gaussian Cube

A Gaussian Cube file (CUB) results from running Cubegen on a Gaussian Checkpoint file. It contains information related to grid data and model coordinates. Gaussian Cube files are supported for import only.

ChemBio3D displays the surface the file describes. If more than one surface is stored in the file, only the first is displayed. You can display additional surfaces using the **Surfaces** menu.

Internal Coordinates

Internal Coordinates (.INT) files are text files that describe a single molecule by the internal coordinates used to position each atom. The serial numbers are determined by the order of the atoms in the file. The first atom has a serial number of 1, the second is number 2, and so on. Internal Coordinates files may be both imported and exported.

You cannot use a Z-matrix to position an atom in terms of a later-positioned or higher serialized atom. If you choose the second or third options in the Internal Coordinates Options dialog box, the nature of the serialization of your model determines whether a consistent Z-matrix can be constructed. If the serial numbers in the Z-matrix which is about to be created are not consecutive, a message appears. You are warned if the atoms in the model must be reserialized to create a consistent Z-matrix.

When you select the Int Coords format, you have several options.

To specify the save options:

1. Click **Save As**.
2. Select the Int. Coords format in the Save As dialog box.
3. Select from these options:

Use Current Z-matrix. Save your model using the Z-matrix described in the Internal Coordinates table of the model.

Only Serial Numbers; Bond and Dihedral Angles. Build a Z-matrix in which the current serial number ordering of the atoms in the model is preserved in the Z-matrix. Pro-R/Pro-S and Dihedral angles are used to position atoms.

Only Serial Numbers; Dihedral Angles Only. Build a Z-matrix in which the current serial number ordering of the atoms in the model is preserved in the Z-matrix. The Pro-R and Pro-S stereochemical designations are not used in constructing the Z-matrix from a model. All atoms are positioned by dihedral angles only.

MacroModel files

The MacroModel[1] (MCM; DAT; OUT) file formats are defined in the MacroModel Structure Files version 2.0 documentation. ChemBio3D supports import of all three file types, and can export MCM

[1]MacroModel is produced within the Department of Chemistry at Columbia University, New York, N.Y.

Maestro files

ChemBio3D 13.0 supports the Schrodinger Maestro file format (MAE) for importing and exporting molecular models.

Molecular Design Limited MolFile

The MDL Molfile format saves files by MDL applications such as ISIS/Draw, ISIS/Base, MAACS and REACCS. The file format is defined in the article, "Description of Several Chemical Structure File Formats Used by Computer Programs Developed at Molecular Design Limited" in the Journal of Chemical Information and Computer Science, Volume 32, Number 3, 1992, pages 244–255.

Use this format to interface with MDL's ISIS applications and other chemistry-related applications. Both import and export are supported.

MSI ChemNote

Use the MSI ChemNote (.MSM) file format to interface with Molecular Simulations applications such as ChemNote. The file format is defined in the ChemNote documentation. Both import and export are supported.

MOPAC Files

MOPAC data may be stored in MOP, DAT, MPC, or 2MT file formats. ChemBio3D can import any of these file formats, and can export MOP files. You can edit MOPAC files using a text editor, adding keywords and changing optimization flags, and run the file using the **Run MOPAC Input file** command within ChemBio3D.

Select **Save All Frames** to create a MOPAC Data file in which the internal coordinates for each view of the model are included. The initial frame of the model contains the first 3 lines of the usual MOPAC output file (see the example file below). Each subsequent frame contains only lines describing the Z-matrix for the atoms in that frame.

Note: *For data file specifications, see the online MOPAC manual.*

To edit a file to run using the Run MOPAC Input File command:

1. Open the MOPAC output file in a text editor.

The output file below shows only the first four atom record lines. The first line and column of the example output file shown below are for purposes of description only and are not part of the output file.

	Col.1	Col. 2	C3	Col. 4	C5	Col. 6	Col. 7	Col. 8		
Line 1										
Line 2	Cyclohexanol									
Line 3										
Line 4	C	0	0	0	0	0	0	0	0	0
Line 5	C	1.54152	1	0	0	0	0	1	0	0
Line 6	C	1.53523	1	111.77	1	0	0	2	1	0
L7.Ln	C	1.53973	1	109.7	1	-55.69	1	1	2	3
Ln+1										

2. In Line 1, type the keywords for the computations you want MOPAC to perform (blank in the example above). Line 2 is where enter the name that you want to assign to the window for the resulting model. However, ChemBio3D ignores this line.

3. Leave Line 3 blank.
4. Line 4 through Ln (were n is the last atom record) include the internal coordinates, optimization flags, and connectivity information for the model.
   - Column 1 is the atom specification.
   - Column 2 is the bond distance (for the connectivity specified in Column 8).
   - Column 3 is the optimization flag for the bond distance specified in Column 2.
   - Column 4 is the bond angle (for the connectivity specified in Column 8).
   - Column 5 is the optimization flag for the bond angle specified in Column 4.
   - Column 6 is the dihedral angle (for the connectivity specified in Column 8).
   - Column 7 is the optimization flag for the dihedral angle specified in Column 6.
5. To specify particular coordinates to optimize, change the optimization flags in Column 3, Column 5 and Column 7 for the respective internal coordinate. The available flags in MOPAC are:

1	Optimize this internal coordinate
0	Do not optimize this internal
-1	Reaction coordinate or grid index
T	Monitor turning points in DRC

6. Add additional information in line Ln+1. For example, symmetry information used in a SADDLE computation.
7. Leave the last line in the data file blank to indicate file termination.
8. Save the file in a text only format.

MOPAC Graph files

A MOPAC Graph (GPT) file stores the results of MOPAC calculations that include the GRAPH keyword. It contains the final geometry, electronic structure, and other properties of the molecule. ChemBio3D supports the MOPAC Graph file format for import only.

Protein Data Bank files

Brookhaven Protein Data Bank files (PDB; ENT) are used to store protein data and are typically large in size. The PDB format provides the primary sequence of protiens. ChemBio3D can import PDB and ENT file types, and export PDB. The PDB file format is taken from the Protein Data Bank Atomic Coordinate and Bibliographic Entry Format Description.

ROSDAL Files (RDL)

The ROSDAL Structure Language[1] (RDL) file format is defined in Appendix C: ROSDAL Syntax of the MOLKICK User's Manual, and in this manual in "File Formats" on page 250. The ROSDAL format is primarily used for query

[1] ROSDAL is a product of Softron, Inc.

searching in the Beilstein Online Database. ChemBio3D supports the ROSDAL file format for export only.

Standard Molecular Data (SMD)
Use the Standard Molecular Data (.SMD) file format for interfacing with the STN Express application for online chemical database searching. Both import and export are supported.

SYBYL files
Use the SYBYL© (SML, SM2, ML2) file formats to interface with Tripos's SYBYL applications. The SML and SM2 formats can be used for both import and export; the ML2 format is supported for import only.

Job description file formats

You can use Job description files to save customized default settings for calculations. You can save customized calculations as a Job Description file (.JDF) or Job Description Stationery (.JDT). Saving either format in a Chem3D job folder adds it to the appropriate Chem3D menu.

JDF files
The JDF file format is a file format for saving job descriptions. When you open a JDF file, you can edit and save the settings.

JDT files
The JDT file format is a template format for saving settings that can be applied to future calculations. You can edit the settings of a template file, however you cannot save your changes.

References

MEP

The Molecular Electrostatic Potential (MEP) is the potential energy of a proton near a molecule. The MEP is typically visualized by mapping the MEP values onto the surface reflecting the molecules boundaries. This surface, called electron density surface, is obtained by plotting the points where the electron density of the molecule's wave function has a constant value.

Electron density is the measure of the probability of an electron being present at a specific location. It is calculated using the formula:

$$\rho(r) = \sum_{\mu}\sum_{\nu} P_{\mu\nu}\phi_{\mu}(r)\phi_{\nu}(r)$$

Where:

- $\rho(r)$, electron density, is a function of the coordinates 'r' and is defined so that '$\rho(r)dr$' is the number of electrons in a small volume, 'dr'.
- $\phi_{\mu}(r)$ and $\phi_{\upsilon}(r)$ are basis functions.
- P is the density matrix.

The density matrix is a self-adjoint positive-semidefinite matrix of trace one that describes the statistical state of a quantum system.

Density matrix is given by the formula:

$$\rho = \sum_{j} p_j |\psi_j > ? < \psi_j|$$

Where:

- ρ is the density operator, which is interchangeably used with density matrix
- coefficients p_j are non-negative and add up to one.
- $|\psi_j>$ is state of the quantum system

You can calculate molecular properties, such as electron density or spin density for a regular grid of points in space and save it as a cube file.

A cube file is a binary or ASCII file that is used as an input for other graphical visualization programs, such as ChemBio3D.

MM2 references

This section provides additional information about the MM2 parameters and force field that has not be covered in other areas of the ChemBio3D 13.0 documentation.

MM2 parameters

The MM2 parameters were derived from three sources:

- Most of the parameters were provided by Dr. N. L. Allinger.
- Several additional parameters were provided by Dr. Jay Ponder, author of the TINKER program.
- Some commonly used parameters that were not provided by Dr. Allinger or Dr. Ponder are provided by Perkin Elmer. However, most of these parameters are estimates which are extrapolated from other parameters.

The best source of information on the MM2 parameter set is *Molecular Mechanics*, Burkert, Ulrich and Allinger, Norman L., ACS Monograph 177, American Chemical Society, Washington, DC, 1982.
A method for developing reasonable guesses for parameters for non-MM2 atom types can be found in “Development of an Internal Searching Algorithm for Parameterization of the MM2/MM3 Force Fields”, Journal of Computational Chemistry, Vol 12, No. 7, 844-849 (1991).

The MM2 force field

ChemBio3D 13.0 includes a new implementation of Norman L. Allinger’s MM2 force field based in large measure on work done by Jay W. Ponder of Washington University. This chapter does not attempt to completely describe the MM2 force field, but discusses how the MM2 force field is used in ChemBio3D and the differences between this implementation, Allinger’s MM2 program (QCPE 395), and Ponder’s TINKER system (M.J. Dudek and J.W. Ponder, *J. Comput. Chem.*, **16**, 791-816 (1995)).
For a review of MM2 and applications of molecular mechanics methods in general, see *Molecular Mechanics*, by U. Burkert and N. L. Allinger, ACS, Washington, D.C., USA, 1982. *Computational Chemistry*, by T. Clark, Wiley, N.Y., USA, 1985, also contains an excellent description of molecular mechanics.
For a description of the TINKER system and the detailed rationale for Ponder’s additions to the MM2 force field, visit the TINKER home page.
For a description and review of molecular dynamics, see *Dynamics of Proteins and Nucleic Acids*, J. Andrew McCammon and Stephen Harvey, Cambridge University Press, Cambridge, UK, 1987. Despite its focus on biopolymers, this book contains a cogent description of molecular dynamics and related methods, as well as information applicable to other molecules.

Allinger’s force field

The ChemBio3D implementation of the Allinger Force Field differs in these areas:

- A charge-dipole interaction term
- A quartic stretching term
- Cutoffs for electrostatic and van der Waals terms with a fifth-order polynomial switching function

- Automatic pi system calculation when necessary

Charge-Dipole interaction term. Allinger's potential function includes one of two possible electrostatic terms: one based on bond dipoles, or one based on partial atomic charges. The addition of a charge-dipole interaction term allows for a combined approach, where partial charges are represented as bond dipoles, and charged groups, such as ammonium or phosphate, are treated as point charges.

Quartic stretching term. With the addition of a quartic bond stretching term, troublesome negative bond stretching energies which appear when long bonds are treated by Allinger's force field are eliminated.
The quartic bond stretching term is required primarily for molecular dynamics; it has little or no effect on low energy conformations.
To precisely reproduce energies obtained with Allinger's force field, set the quartic stretching constant in the MM2 Constants table window to zero.

Electrostatic and van der Waals cutoff terms. The cutoffs for electrostatic and van der Waals terms greatly improve the computation speed for large molecules by eliminating long range interactions from the computation.
To precisely reproduce energies obtained with Allinger's force field, set the cutoff distances to large values (greater than the diameter of the model).

The cutoff is implemented gradually, beginning at 50% of the specified cutoff distance for charge and charge-dipole interactions, 75% for dipole-dipole interactions, and 90% for van der Waals interactions. ChemBio3D uses a fifth-order polynomial switching function so that the resulting force field is second-order continuous.
Because the charge-charge interaction energy between two point charges separated by a distance r is proportional to 1/r, the charge-charge cutoff must be rather large, typically 30 or 40Å. The charge-dipole, dipole-dipole, and van der Waals energies, which fall off as $1/r^2$, $1/r^3$, and $1/r^6$, respectively, can be cut off at much shorter distances, for example, 25Å, 18Å, and 10Å, respectively. Fortunately, since the van der Waals interactions are by far the most numerous, this cutoff speeds the computation significantly, even for relatively small molecules.

Pi Orbital SCF computation. ChemBio3D determines whether the model contains any pi systems, and performs a Pariser-Parr-Pople pi orbital SCF computation for each system. A pi system is defined as a sequence of three or more atoms of types which appear in the Pi Atoms table window (PIATOMS.xml) .
The method used is that of D.H. Lo and M.A. Whitehead, *Can. J. Chem.*, 46, 2027 (1968), with heterocycle parameters according to G.D. Zeiss and M.A. Whitehead, *J. Chem. Soc. (A)*, 1727 (1971). The SCF computation yields bond orders which are used to scale the bond stretching force constants, standard bond lengths, and twofold torsional barriers.

A step-wise overview of the process used to perform pi system calculations is as follows:

1. A matrix called the Fock matrix is initialized to represent the favorability of sharing electrons between pairs of atoms in a pi system.
2. The pi molecular orbitals are computed from the Fock matrix.
3. The pi molecular orbitals are used to compute a new Fock matrix, then this new Fock matrix is used to compute better pi molecular orbitals.
4. Step 2 and step 3 are repeated until the computation of Fock matrix and the pi molecular orbitals converge. This method is called the self-consistent field technique or a pi-SCF calculation.
5. A pi bond order is computed from the pi molecular orbitals.
6. The pi bond order is used to modify the bond length (BL_{res}) and force constant (KS_{res}) for each sigma bond in the pi system.
7. The values of KS_{res} and BL_{res} are used in the molecular mechanics portion of the MM2 computation to further refine the molecule.

To examine the computed bond orders after an MM2 computation:

1. In the Pop-up Information control panel, select Bond Order.
2. Position the pointer over a bond.

The information box contains the newly computed bond orders for any bonds that are in a pi system.

CS MOPAC

This section provides additional information about the MOPAC that has not be covered in other areas of the ChemBio3D 13.0 documentation:

- Potential energy functions
- Adding parameters to MOPAC
- Electronic configuration (includes using MOPAC sparkles)

ChemBio3D 13.0 supports MOPAC 2007 and MOPAC 2009.

Potential energy functions

MOPAC provides five potential energy functions: MNDO, PM3, PM6, AM1, and MNDO-d. All are SCF (Self Consistent Field) methods. Each function represents an approximation in the mathematics for solving the Electronic Schrödinger equation for a molecule.

Historically, these approximations were made to allow *ab initio* calculations to be within the reach of available computer technology. Currently, *ab initio* methods for small molecules are within the reach of desktop computers. Larger molecules, however, are still more efficiently modeled on the desktop using semi-empirical or molecular mechanics methodologies.

To understand the place that the potential energy functions in MOPAC take in the semi-empirical arena, here is a brief chronology of the approximations that comprise the semi-empirical methods. The first approximation was termed CNDO for Complete Neglect of Differential Overlap. The next approximation was termed INDO for Intermediate Neglect of Differential Overlap, Next followed MINDO/3, which stands for “Modified Intermediate Neglect of Differential

Overlap". Next was MNDO, which is short for "Modified Neglect of Differential Overlap" which corrected MINDO/3 for various organic molecules made up from elements in rows 1 and 2 of the periodic table. AM1 improved upon MNDO markedly. Finally the most recent, PM3 is a reparameterization of AM1. The approximations in PM3 are the same as AM1.
This sequence of potential energy functions represents a series of improvements to support the initial assumption that complete neglect of diatomic orbitals would yield useful data when molecules proved too resource intensive for *ab initio* methods.

Adding parameters to MOPAC

Parameters are in constant development for use with PM3 and AM1 potential functions. If you find that the standard set of parameters that comes with CS MOPAC does not cover an element that you need, for example Cu, you can search the literature for the necessary parameter and add it at run time when performing a MOPAC job. This flexibility greatly enhances the usefulness of MOPAC.
You can add parameters at run time using the keyword EXTERNAL=name, where name is the name of the file (and its full path) containing the additional parameters.

Using keywords

Selecting parameters for a MOPAC approximation automatically inserts keywords in a window on the **General** tab of the MOPAC Interface. You can edit these keywords or use additional keywords to perform other calculations or save information to the *.out file.

Caution: *Use the automatic keywords unless you are an advanced MOPAC user. Changing the keywords may give unreliable results.*

For a complete list of keywords see the MOPAC online manual.

Automatic keywords

The following contains keywords automatically sent to MOPAC and some additional keywords you can use to affect convergence.

Keyword	Description
EF	Automatically sent to MOPAC to specify the use of the Eigenvector Following (EF) minimizer.
BFGS	Prevents the automatic insertion of EF and restores the BFGS minimizer.
GEO-OK	Automatically sent to MOPAC to override checking of the Z-matrix.
MMOK	Automatically sent to MOPAC to specify Molecular Mechanics correction for amide bonds. Use the additional keyword NOMM to turn this keyword off.
RMAX=n.nn	The calculated/predicted energy change must be less than n.nn. The default is 4.0.
RMIN=n.nn	The calculated/predicted energy change must be more than n.n. The default value is 0.000.
PRECISE	Runs the SCF calculations using a higher precision so that values do not fluctuate from run to run.
LET	Overrides safety checks to make the job run faster.
RECALC=5	Use this keyword if the optimization has trouble converging to a transition state.

For descriptions of error messages reported by MOPAC see the MOPAC manual.

Additional keywords

Keywords that output the details of a particular computation are shown in the following table. Terms marked with an asterisk (*) appear in the *.out file.

Keyword	Data
ENPART	All Energy Components*
FORCE	Zero Point Energy
FORCE	Vibrational Frequencies*
MECI	Microstates used in MECI calculation*
none	HOMO/LUMO Energies*
none	Ionization Potential*
none	Symmetry*
LOCALIZE	Print localized orbitals
VECTORS	Print final eigenvectors (molecular orbital coefficients)
BONDS	Bond Order Matrix*

The following table contains the keywords that invoke additional computations. Terms marked with an asterisk (*) appear in the *.out file.

Keyword	Description
CIS	UV absorption energies* Performs C.I. using only the first excited Singlet states and does not include the ground state. Use *MECI* to print out energy information in the *.out file.
FORCE	Vibrational Analysis*Useful for determining zero point energies and normal vibrational modes. Use *DFORCE* to print out vibration information in *.out file.
NOMM	No MM correction By default, MOPAC performs a molecular mechanics (MM) correction for CONH bonds.
PI	Resolve density matrix into sigma and pi bonds.
PRECISE	Increase SCF criteria Increases criteria by 100 times. This is useful for increasing the precision of energies reported.
T = n [M,H,D]	Increase the total CPU time allowed for the job. The default is 1h (1 hour) or 3600 seconds.

Specifying electronic configuration

MOPAC must have the net charge of the molecule in order to determine whether the molecule is open or closed shell. If a molecule has a net charge, be sure you have either specified a charged atom type or added the charge.
You can assign a charge using the Build from Text tool or by specifying it in MOPAC:
To add the charge to the model:

1. Click the Build from Text tool.
2. Click an atom in your model.
3. Type a charge symbol.

For example, click a carbon and type “+” in a text box to make it a carbocation.The charge is automatically sent to MOPAC when you do a calculation.
To specify the charge in MOPAC:

1. Go to **Calculations**>**MOPAC Interface** and choose a calculation. The MOPAC Interface dialog box appears.
2. On the **General** tab, in the **Keywords** box, type the keyword CHARGE=n, where n is a positive or negative integer (-2, -1, +1, +2).

Different combinations of spin-up (alpha electrons) and spin-down (beta electrons) lead to various electronic energies. These combinations are specified as the Spin Multiplicity of the molecule. The following table shows the relation between total spin S, spin multiplicity, and the number of unpaired electrons.

Spin	Keyword	(# unpaired electrons)
0	SINGLET	0 unpaired
1/2	DOUBLET	1 unpaired
1	TRIPLET	2 unpaired
1 1/2	QUARTET	3 unpaired
2	QUINTET	4 unpaired
2 1/2	SEXTET	5 unpaired

To determine the appropriate spin multiplicity, consider whether:

- The molecule has an even or an odd number of electrons.
- The molecule is in its ground state or an excited state.
- To use RHF or UHF methods.

The following table shows some common permutations of these three factors:

RHF (Closed Shell)

Electronic State	Keywords to Use[a]			
Ground	SINGLET			
	DOUBLET	1,2		
	TRIPLET	2,2		
	QUARTET	3,3		
	QUINTET	4,4		

[a] **Do not use OPEN(n1,n2) for ground-state systems except for high symmetry systems with open shells**

Electronic State	Keywords to Use[a]			
	SEXTET	5,5		
1st Excited	SINGLET		2	
	DOUBLET		2	2
	TRIPLET		2	3
	QUARTET		2	4
	QUINTET		2	5
	SEXTET		2	6
2nd Excited	SINGLET		3	
	DOUBLET		3	3
	TRIPLET		3	3
	QUARTET		3	4
	QUINTET		3	5
	SEXTET		3	6

UHF (Open Shell)	
Electronic State	**Spin State**
Ground	SINGLET
	DOUBLET
	TRIPLET
	QUARTET
	QUINTET
	SEXTET

[a]Do not use OPEN(n1,n2) for ground-state systems except for high symmetry systems with open shells

Even-electron systems

If a molecule has an even number of electrons, the ground state and excited state configurations can be Singlet, Triplet, or Quintet (not likely). Normally the ground state is Singlet, but for some molecules, symmetry considerations indicate a Triplet is the most stable ground state.

Ground State, RHF . The Ground State, RHF configuration is as follows:

Singlet ground state. the most common configuration for a neutral, even electron stable organic compound. No additional keywords are necessary.

Triplet ground state. Use the following keyword combination: TRIPLET OPEN(2,2)

Quintet ground state. Use the following keyword combination: QUINTET OPEN(4,4)

Note: *The OPEN keyword is normally necessary only when the molecule has a high degree of symmetry, such as molecular oxygen. The OPEN keyword increases the active space available to the SCF calculation by including virtual orbitals. This is necessary for attaining the higher multiplicity configurations for even shell system. The OPEN keyword also invokes the RHF computation using the 1/2 electron approximation method and a C.I. calculation to correct the final RHF energies. To see the states used in a C.I. calculation, type MECI as an additional keyword. The information is printed at the bottom of the *.out file.*

Ground State, UHF. For UHF computations, all unpaired electrons are forced to be spin up (alpha).

- Singlet ground state—the most common configuration for a neutral, even electron, stable organic compound. No additional keywords are necessary.
- UHF will likely converge to the RHF solution for Singlet ground states.
- Triplet or Quintet ground state: Use the keyword TRIPLET or QUINTET.

Note: *When a higher multiplicity is used, the UHF solution yields different energies due to separate treatment of alpha electrons.*

Excited State, RHF. First Excited State: The first excited state is actually the second lowest state (the root=2) for a given spin system (Singlet, Triplet, Quintet).

To request the first excited state, use the following sets of keywords:

First excited Singlet: ROOT=2 OPEN(2,2) SINGLET (or specify the single keyword EXCITED)

First excited triplet: ROOT=2 OPEN (2,2)TRIPLET C.I.=n

, where n=3 is the simplest case.

First excited quintet: ROOT=2 OPEN (4,4) QUINTET C.I.=n, where n=5 is the simplest case.

Second Excited State: The second excited state is actually the third lowest state (the root=3) for a given system (Singlet, Triplet, Quintet). To request the second excited state use the following set of keywords:

Second excited Singlet: OPEN(2,2) ROOT=3 SINGLET

Second excited triplet: OPEN(2,2) ROOT=3 TRIPLET C.I.=n, where n=3 is the simplest case.

Second excited quintet: OPEN(4,4) ROOT=3 QUINTET C.I.=n, where n=5 is the simplest case.

Excited State, UHF. Only the ground state of a given multiplicity can be calculated using UHF.

Odd-electron systems

Often, anions, cations, or radicals are odd-electron systems. Normally, the ground states and excited state configuration can be doublet, quartet or sextet.

Ground State, RHF

Doublet ground state: This is the most common configuration. No additional keywords are necessary.

Quartet: Use the following keyword combination: QUARTET OPEN(3,3)

Sextet ground state: Use the following keyword combination: SEXTET OPEN(5,5)

Ground State, UHF

For UHF computations all unpaired electrons are forced to be spin up (alpha).

Doublet ground state: This is the most common configuration for a odd electron molecule. No additional keywords are necessary.

UHF will yield energies different from those obtained by the RHF method.

Quartet and Sextet ground state: Use the keyword QUARTET or SEXTET.

Excited State, RHF. First Excited State: The first excited state is actually the second lowest state (the root=2) for a given spin system (Doublet, Quartet, Sextet). To request the first excited state use the following sets of keywords.

First excited doublet: ROOT=2 DOUBLET C.I.=n, where n=2 is the simplest case.

First excited quartet: ROOT=2 QUARTET C.I.=n, where n=4 is the simplest case.

First excited sextet: ROOT=2 SEXTET C.I.=n, where n=5 is the simplest case.

Second Excited State: The second excited state is actually the third lowest state (the root=3) for a given system (Singlet, Triplet, Quintet). To request the second excited state use the following set of keywords:

Second excited doublet: ROOT=3 DOUBLET C.I.=n, where n=3 is the simplest case.

Second excited quartet: ROOT=3 QUARTET C.I.=n, where n=4 is the simplest case.

Second excited sextet: ROOT=3 SEXTET C.I.=n, where n=5 is the simplest case.

Note: *If you get an error indicating the active space is not spanned, use C.I.> n for the simplest case to increase the number of orbitals available in the active space. To see the states used in a C.I. calculation, type MECI as an additional keyword. The information is printed at the bottom of the *.out file.*

Excited State, UHF. Only the ground state of a given multiplicity can be calculated using UHF.

Sparkles

Sparkles are used to represent pure ionic charges. They are roughly equivalent to the following chemical entities:

Chemical symbol	Equivalent to...
+	tetramethyl ammonium, potassium or cesium cation + electron
++	barium di-cation + 2 electrons
_	borohydride halogen, or nitrate anion minus electron
=	sulfate, oxalate di-anion minus 2 electrons

Sparkles are represented in ChemBio3D 13.0 by adding a charged dummy atom to the model.

Tip: *Dummy atoms are created with the uncoordinated bond tool. You must add the charge after creating the dummy.*

The output file shows the chemical symbol as XX.

Approximate Hamiltonians in MOPAC

There are five approximation methods available in CS MOPAC:

- MNDO
- AM1
- PM3
- PM6
- MNDO-d

The potential energy functions modify the HF equations by approximating and parameterizing aspects of the Fock matrix.

The approximations in semiempirical MOPAC methods play a role in the following areas of the Fock operator:

- The basis set used in constructing the 1-electron atom orbitals is a minimum basis set of only the s and p Slater Type Orbitals (STOs) for valence electrons.
- The core electrons are not explicitly treated. Instead they are added to the nucleus. The nuclear charge is termed Neffective.

  For example, Carbon as a nuclear charge of +6-2 core electrons for a effective nuclear charge of +4.
- Many of the 2-electron Coulomb and Exchange integrals are parameterized based on element.

Choosing a Hamiltonian

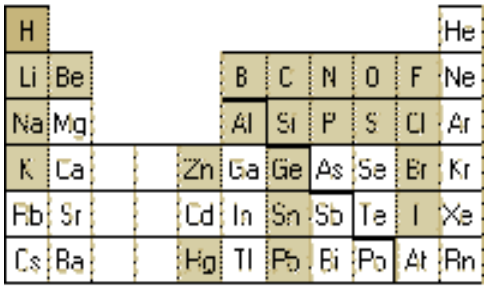
Overall, these potential energy functions may be viewed as a chronological progression of improvements from the oldest method, MINDO/3 to the newest method, PM6. However, although the improvements in each method were designed to make global improvements, they have been found to be limited in certain situations.
The two major questions to consider when choosing a potential function are:

- Is the method parameterized for the elements in the model?
- Does the approximation have limitations which render it inappropriate for the model being studied?

For more detailed information see the MOPAC online manual.

MNDO applicability and limitations

MNDO may be applied to the shaded elements in the table below:

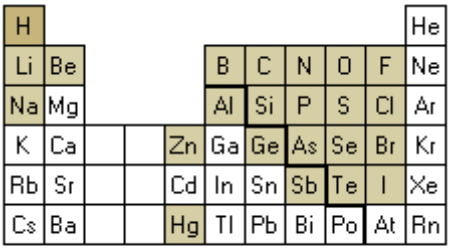


The following limitations apply to MNDO:

- Sterically crowded molecules, such as neopentane, are too unstable.
- Four-membered rings, such as in cubane, are too stable.
- Hydrogen bonds are virtually non-existent, for example, water dimer. Overly repulsive nonbonding interactions between hydrogens and other atoms are predicted. In particular, simple hydrogen bonds are generally not predicted to exist using MNDO.
- Hypervalent compounds, such as sulfuric acid are too unstable.
- Activation barriers are generally too high.
- Non-classical structures are predicted to be unstable relative to the classical structure, for example, ethyl radical.
- Oxygenated substituents on aromatic rings are out-of-plane, for example, nitrobenzene.
- • The peroxide bond is systematically too short by about 0.17 Å.
- • The C-O-C angle in ethers is too large.

AM1 applicability and limitations

AM1 may be applied to the shaded elements in the table below:

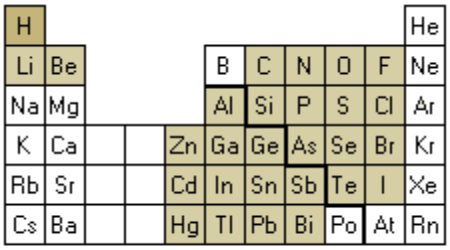


Important factors relevant to AM1 are:

- AM1 is similar to MNDO; however, there are changes in the core-core repulsion terms and reparameterization.
- AM1 is a distinct improvement over MNDO, in that the overall accuracy is considerably improved. Specific improvements are:
  - The strength of the hydrogen bond in the water dimer is 5.5 kcal/mol, in accordance with experiment.
  - Activation barriers for reaction are markedly better than those of MNDO.
  - Hypervalent phosphorus compounds are considerably improved relative to MNDO.
  - In general, errors in ΔH_f obtained using AM1 are about 40% less than those given by MNDO.
  - AM1 phosphorus has a spurious and very sharp potential barrier at 3.0Å. The effect of this is to distort otherwise symmetric geometries and to introduce spurious activation barriers. A good example is given by P4O6, in which the nominally equivalent P-P bonds are predicted by AM1 to differ by 0.4Å. This is by far the most severe limitation of AM1.
  - Alkyl groups have a systematic error due to the heat of formation of the CH2 fragment being too negative by about 2 kcal/mol.
  - Nitro compounds, although considerably improved, are still systematically too positive in energy.
  - The peroxide bond is still systematically too short by about 0.17Å.

PM3 applicability and limitations

Parameterized Model revision 3 (PM3) may be applied to the shaded elements in the following table:



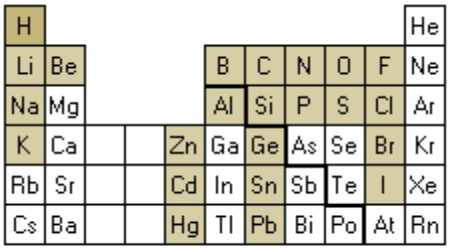
The following apply to PM3:

- PM3 is a reparameterization of AM1.

- PM3 is a distinct improvement over AM1.
- Hypervalent compounds are predicted with considerably improved accuracy.
- Overall errors in ΔH_f are reduced by about 40% relative to AM1.
- Little information exists regarding the limitations of PM3. This should be corrected naturally as results of PM3 calculations are reported.
- The barrier to rotation in formamide is practically non-existent. In part, this can be corrected by the use of the MMOK option. For more information about MMOK see the online MOPAC Manual.

MNDO-d applicability and limitations

Modified Neglect of Differential Overlap with d-Orbitals (MNDO-d) may be applied to the shaded elements in the table below:



MNDO-d is a reformulation of MNDO with an extended basis set to include d-orbitals. This method may be applied to the elements shaded in the table below. Results obtained from MNDO-d are generally superior to those obtained from MNDO. The MNDO method should be used where it is necessary to compare or repeat calculations previously performed using MNDO.
The following types of calculations, as indicated by MOPAC keywords, are incompatible with MNDO-d:

- COSMO (Conductor-like Screening Model) solvation
- POLAR (polarizability calculation)
- GREENF (Green's Function)
- TOM (Miertus-Scirocco-Tomasi self-consistent reaction field model for solvation)

PM6 applicability and limitations

Parameterized Model revision 6 (PM6) may be applied to all main group elements and transition metals.
The following apply to:

- PM6 is a reparameterization of PM5. It has been developed using experimental and *ab initio* data from over 9000 compounds.
- PM6 is a distinct improvement over PM3 and AM1.
- Corrects major errors in AM1 and PM3.
- More accurate prediction of heat of formation.

- Generates more accurate geometries- For example, it optimizes anthraquinones to correct planar fused ring structure.
- More accurate positioning of bridging hydrogen bonds- for example, the bridging hydrogen bond between the two oxygen atoms is positioned equidistant in dicarboxylic acid anions.

Online Resources

PerkinElmer provides several online resources of information to help you get the most out of ChemBio3D 13.0. Everything listed below is available under **Online** in the ChemBio3D 13.0 main menu.

SciStore

Go to **Online**>**Browse SciStore.com.**

Scistore.com offers a variety of full products, plugins, and upgrades for the scientific community. For molecular modeling and other software, visit the SciStore Web site and go to **Software**>**Chemistry**>**Molecular Modeling** in the SciStore main menu.

PerkinElmer Informatics

Go to **Online**>**Browse CambridgeSoft.com.**

See the PerkinElmer Informatics Web site for the latest software, databases, services, video tutorials, and much more.

Online documentation

Go to **Online**>**Browse CambridgeSoft Documentation**

Download and view documentation for allof our software products.

Online registration

Go to **Online**>**Register Online.**

Register your copy ChemBio3D and your other software.

ChemOffice SDK

Go to **Online**>**Browse ChemOffice SDK.**

Refer to the SDK for documentation, sample code, and other resources for the ChemOffice component APIs.

Troubleshooting

This section describes steps you can take that affect the overall performance of CS Desktop Applications, as well as steps to follow if your computer crashes when using a CS software product.

Performance

Below are some ways you can optimize the performance of ChemBioOffice Desktop Applications:

- In the Performance tab in the System control panel, allocate more processor time to the application.
- Install more physical RAM. The more you have, the less ChemBioOffice Desktop Applications will have to access your hard disk to use Virtual Memory.

- Increase the Virtual Memory (VM). Virtual memory extends RAM by allowing space on your hard disk to be used as RAM. However, the time for swapping between the application and the hard disk is slower than swapping with physical RAM.

Applications and Drivers

As with most complex software applications, there may be unusual circumstances in which ChemBio3D may become unresponsive. Below are some recommended steps for you to follow to try to resolve software and driver issues.

1. Restart Windows and try to reproduce the problem. If the problem recurs, continue with the following steps.
2. The most common conflicts concern video drivers, printer drivers, screen savers, and virus protection. If you do need to contact us, be sure to determine what type and version of drivers you are using.

- **Video Driver related problems:** If you have problems displaying any ChemBioOffice Desktop Application, try switching to the VGA video driver in the display Control Panel or System Setup, and then retest the problems. If using a different driver helps, your original driver may need to be updated–contact the maker of the driver and obtain the most up-to-date driver. If you still have trouble contact us with the relevant details about the original driver and the resulting problem.
- **Printer Driver related problems:** Try using a different printer driver. If using a different driver helps, your original driver may need to be updated–contact the maker of the driver and obtain the most up-to-date driver. If you still have trouble contact us with the relevant details about the original driver and the resulting problem.

3. Try reinstalling the software. Before you reinstall, uninstall the software and disable all background applications, including screen savers and virus protection. See the complete uninstall instructions on the Technical Support web page.
4. If the problem still occurs, use our online contact form and provide the details of the problem to Technical Support.

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